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<p>(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,
5 the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence
25 amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the
amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15 $p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 $\text{cum } p(\text{ID}) = p(\text{ID1})p(\text{ID2})p(\text{ID3})\dots p(\text{IDn})$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded).

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

WI-9651b	105 A T ---	---	TCCTACATCTATGGACAACTCCATGCCCTTTGCACATGCTGATCCCTCCCTCCTGGAATCCTTTCTCT ACTTGCTCCTCATGTACAAATTTCTGCTGCTCTTCAATJGGGGCAGCTTGAAGCCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTATAGGCCTCTG TCCTTAACTGTAAATGGTATATTAACTCTGGTGTTGAATGCTCTC
WI-9651	139 T C ---	---	TCCTACATCTATGGACAACTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATCCTTTCTCT ACTTGCTCCTCATGTACAAATTTCTGCTGCTCTTCAAGGGGAGCTTGAAGCCCTCCCTTTAGACACCT CTTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTATAGGCCTCTGT CTTAAACCTGTAAATGGTATATTAACTCTGGTGTTGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAACTCTTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGCTCTCTTGGTCCCTGCTGGTTCAGGGGAGAGCGGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCTGGAGGCACTATAGGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAACTCTTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGGCTCTCTTGGTCCCTGCTGGTTCAGGGGAGAGCGGTGGACTGCAGCTTCTGCTGGTGC GTGCTCCCCCGTCTCTGGAGGCACTATAGGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGTCTGTTCATTCTCTCTCTCCAATGAAGGATATTTAAGCATCATT CATCTGGCCCTTTTGGAGTTTGAATATTTTGTGATGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTATCTTTTGTATAGGAGTTTGGCCATGACCTTTATGAGGAGAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42 T C ---	---	TTGGTGTGAATCAGAATATAGGAAATAGACAATTTGAA/T/A.CGTACCCCGAGAAACAAGAG CCCTGCACCTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCAGACTTTATTTGATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCTCCCTCCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTTCAGAGAGCTGAAAGGGTCCCTCGGCTCTTTATTT CAGGGCTTTGCATGCGCTCTATTCCTCTGCTGCTCTC/AJCCACCTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGATCACCACCTCACTAAATATCAACTTATGTGTATCAGATATCCTCTCT ACCCTCAGCTTATTTGAAGAAATCCTAAACATCAAACTTTCATCCATAAAATGTACGATTTT /CJA TAAAAACAATAAATTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---			---	TCCTATTTCACAGTAGCCCCATGAAGTAGGTAAACCAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGCTCAGGTTTTCTTAATAAGCAAAGACCTGCAJVC JCCCTGGCTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---			---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACCTTTGGAGATTCATTTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAAGAACTTTGTGGGTATAGAAATGGAATGGAGATTTCAACAGCTTTGCTGAAAC TGACTTTGG[G]AJCTCCAGACTTCACCTGCTCCTTAGGCATTGAAACCATCACCTGGTTGCACTTCTC ATGACTGAGGTTAAGTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T --			---	AAACACACAGAATCATCAAAGCACAJTATCTGTGTTTGAGATAAATGATAGCTGAGTCACCTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAATTTTCATTCTATGAAACCTCCCCATACTGT AATTGGACAGTTTGTGTTCCAC
WI-4687	121 G T ---			---	TAGTATGCTACTGCCATGGTAAGGACTTTGATCACTAGGAATAAAGAACACTTTGAATGGTCTTGTCO TTTCAATAAAAAAGAGTGACATGATTGAACATGTGTTTTAGATAAAGGGCACTT[G]TGCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAACTTGTAT
WI-4719b	107 T G ---			---	TTCAATTTCCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTTGGGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTAGAGTTTACAGAGTTGACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---			---	TTCAATTTCCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTTGGGTGAGCGGATT AT[G]AJCTGACGCCATGGGTTCATAAGTGACTTAGAGTTTACAGAGTTTACAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---			---	TCAACACGCTTTTATGGCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACCTTCTCTGCACACTGCCAAGT TAAAGAAAACCCCTGCTTGTCTGGAGAGGGAGGGGCAGACAGGGGAATTCAGGGGCATGTATGGCTC AGTCCCACTTCT[G]AJCTGCAGAGTATAGGGACCAAGGTTCCAAACTTT
WI-9484	178 G A ---			---	TCAACACGCTTTTATGGCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACCTTCTCTGCACACTGCCAAGT TAAAGAAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGG[G]AJAGGAATTCAGGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAAGGTTCCAAACTTT

WI-7330	207	CT	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAGTCATACTTTGGTGGCTAAGTTTACTAAGGAAAATAACTGAAAAAGATTAAAAAG TGAGAGTC/TTGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACACAG
WI-9443	211	GA	---	---	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACATT GCACAAATTAATCTCTTGGCATCATACAAACTGGTTTTAATGGCAAAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCATACGCTCACACCTGAGGGGAAGGCACCTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCCACTT
WI-7166	59	CT	---	---	TCCTCTAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCTTCTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGGTTTAACTTGTGCTGTGAACAAATGTGCGAAAAAGAGTCTTCCAAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	TC	---	---	GCTTCTCCCCAGGAAGCGGGGCTTGGCCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCTCTGCGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/T]GGGGAGCAG AGCCACAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188	GT	---	---	GCTTCTCCCCAGGAAGCGGGGCTTGGCCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCTCTGCGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[C/G, I]TGGGGGAGCA GAGCCACAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275	AG	---	---	GTACTTTAGGCTGTGGAGGTGGCATTAGTGGTGACCCCTGCACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCATATG GCCATAAACTGCCTAAGCACTCAGGCCCTCCACTCATCAACCCCTTTGACCCAGAGAAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCTCTGGCTG
WI-7685	46	TC	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTC[T/C]TTTCTCCCTCTGGATCA AAGTAGGAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGTACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCTAGCCTTATCCTCTGATCTCCATGGCTCTCTCCCTCCCTCTGCGGACTC CTGGTTGAGCTGTTGCCTCAGTCCCCCAACAGAIGCTTTCTGTCTC
WI-563	87	GA	---	---	TGTGACCAATTGTTATTTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGAGGGCTCCCTT[G/A]CCCTGATCATGTCTACCTAACTGCTTACTCTAACATACTACTCTCC TGTGGTATGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCAGAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGCAAAATGATCCTTCT GTTGCTGCACGTGTCAATTACTGTGTATGGATTTAATATTGTCCAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACACCCCTGGAGTT TCTCTCCCTCCCTA/GJTCCTCACCACACCTTCCAGTGTATTCTGCTGTGCAAAATGATCCT TCTGTTGCTGCACGTGTCAATTACTGTGTATGGATTTAATATTGTCCAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[G/G]GCCACTAGCCCTGAACCTTGACACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGCAAAATGATCCT TCTGTTGCTGCACGTGTCAATTACTGTGTATGGATTTAATATTGTCCAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGAGTGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTACG CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGAGTGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAGA[G/A]CAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTACG CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281 T C ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[G/J]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGAA GAGT[C/A]GTGACTTTATGCCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTGA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTTCAAGG TTAACAGCCACCATTTGTAAACACATTGT

WI-10673	94	C G ---	---	---	TCCCTTTATGCACCCAAAGAGATATTTATTAAACACCAATTTACGTAGCAGGCCATGGCTCATGGGAACC CACCCTCCGTTGGCACTCATGGAGGGG[C/G]TGAGGTTGGAACATATGCAGTGTGCTCCGGCCACACA TCCTGTGGGCCCCCTACCCTGCCCAATTCATCTGCCAATAAATCCTGTCTTATTTGTTTCATCCTG GAGATTGAAGGGAGGTCAAGTTGTTTGCAATGATTTGTCAGAGAACCT
WI-7842	57	T C ---	---	---	CACAGCATGCCCTTGAGGAGCCGCCACAGATGCTGAATCCCTATCCCATTCGT[C/G]GTATGAG TCCCATTTGCCCTTGCAATTAGCATCTGTCTCCCCCAAAAGAAATGTGCTATGAAGCTTTCTTTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAATGATTGAGCTCCCTTATA
WI-7721	145	A C ---	---	---	CTGCCATCATCAGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGCCACATCCCCACCCAGCTGTTACCCAGCCGGGCGAGGTGCAGCCCTTCTCTCC TGCTCTGC[A/C]CTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATCCTCTTACTGGGGCTGGGGCTCTAGCCAA
WI-4767b	173	C A ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGTCTGGTAATCTAGATCTTCTATATCCATTGAGTGTGAGTTGGAGAGAGGTATGTTT CTTGCTTGAGAAATCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCCTACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50	A G ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGAGTTGGAGAGAGGTATG TTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222	C T ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTAIGTATTAAAT
WI-7718e	60	T C ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31	G A ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C]TGTACTCCCTACACTGATGC AAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATT[A]
WI-7227d	99 G C ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCACTTTTCAGACAAAGCTTTA[G/C]JAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCAATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCACTTTTCAGACAA[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCAATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93 G T ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCACTTTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCAATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	CCCAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGCTGGAGGTGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGTATGCTTTCATCGAACAACTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATGATCTTGAGATTTC
WI-7310b	234 A C ---	---	---	

WI-7310a	64 T A ---	---	---	CCACAATGCCCTCTOCCACGATGTCAAGGACTCCTGTCTGTCTGAGGGTGGGAGACAAGGAACQTA JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAACCTGATCGGAA AAGTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAAGTGAAGCAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTG[C/G]TGGTTGATAATCA GATCATGCCAAGACGGCCCTCTGATAATCGCTTGGGCATGATTGCAATGGAGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG[A/G]GTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTGT CTGTGGGAGCCCAGGAAGCTGCTACCCAAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTG[C/G]TGGTTGATAATAA TCAGATCATGCCAAGACGGCCCTCTGATAATCGCTTGGGCATGATTGCAATGGAGGCAATGCG GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTG TCTGTGGGAGCCCAGGAAGCTGCTACCCAAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCTACC AGCCCTGGAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAGATC AGATGTGCCAAGGAAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAAGGCCCTC[C/G]TGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC[C/G]CCTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAG ATCAGATGTGGCAAGGAAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC[C/G]CCTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAG ATCAGATGTGGCAAGGAAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGCACATTCAATCCTGAAACAACCTG CCAGGCAAGTCTCTTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GGATGTAGATTGCACATTCAATCCTGAAACAACCTG CCAGGCAAGTCTCTTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAGGAGTGTGAGGTTTGTCCC

WI-1795b	130	T C	---	---	GAAGCAACCAGAAAGTATCTTATCCCACATCTAGATTATGCTGGGTTCTCCAGACTCCTACGATTAAATGTGATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTCTTTGCAGAAAGAAAGT/CJC GTCTACCATTTTCACCAAATTTTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCTAGGAGTCTAAAGTGAGCTGGGAAGGCAGGATT
WI-1795a	47	T C	---	---	GAAGCAACCAGAAAGTATCTTTATCCCACATCTAGATTATGCTGGGTT/CJCTCCAGACTCCTACGATTAATTTGATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTCTTTGCAGAAAGAAAGTCTAAATTTGATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTCTTTGCAGAAAGAAAGTCTAAATTTTCACCAAATTTTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCTAGGAGTCTAAAGTGAGCTGGGAAGGCAGGATT
WI-10616d	136	G A	---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCCATGTCCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTCTCTATCACATTGGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTTTGT
WI-10616c	136	G A	---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCCATGTCCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTCTCTATCACATTGGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTTTGT
WI-10616b	141	C T	---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCCATGTCCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTCTCTATCACATTGGCCA CGTAGC/CJCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTTTGT
WI-10616a	116	G C	---	---	CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCCATGTCCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTCTCTATCACATTGGCCA CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCCATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTTTGT
WI-1126c	52	G A	---	---	CTCTTATTTCTCTGGGCAGTCTTTCTTTGGGGCAAACTTCCAGTATCACT[G/A]TACTAATAATAA AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAAATATTTAAATTCAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACTTTTTTGGACTTGCTTTATTCTT
WI-1126b	230	T C	---	---	CTCTTATTTCTCTGGGCAGTCTTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAATAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTTCCAGCAAGAAATTT TATTTCTCAAGATATAAAAAATAAAATATTTAAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAAATGCAATCCAGCTGTAACTTTTTT/CJGGACTTGCTTTATTCTT

WI-1126a	97	T C ---			CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATACATAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAGATT/CJCAATATATATCCAGATTGTTTTCCAGCAAGAAAA ATTTTATTTCTCAAGATATAAAAAATAATATTTAAATTCAGTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACATTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T ---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
WI-11183b	192	T C ---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAAT/CJATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
WI-11183a	118	C T ---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
WI-10770b	174	G A ---			GCTTGGTTTGGCTTATGCTTATGCTCAGTCTTGAGTCTCCCTTCTGCCCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTCTCTCTGTACTTTCTCCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA/GAJTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-10770a	49	G T ---			GCTTGGTTTGGCTTATGCTTATGCTCAGTCTTGAGTCTCCCTTCTGCCCTGGCCCTTTTGATTT TCACCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTCTCTCTGTACTTTCTC CTGTTCAACCAACCTTCTTTTATCTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-9667b	82	C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTTGATCATGG TTATCACTGGACA/CJTAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATCT
WI-9667a	68	G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTCTGCCCTTGATCATG G/CJTTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATCT

WI-10400d	189 A G ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACATAATTTTATTCTAATTTT TCITTCCTTACCTTACTCTCCCAACCCCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACATAATTTTATTCTAATTTT TCITTCCTTACCTTACTCTCCCAACCCCA[A/C]JAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACATAATTTTATTCTAATTTT TCITTCCTTACCTTACTCTCCCAACCC[A/G]JAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAAGTAAT[C/J]TGCAATTTTCAGACATCT GCTGGTAACTGTTATAAGATGGTTTAGCACACATGTAGCAGCTTACTAACACATAATTTTATTCTA ATTTTCITTCCTTACCTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA[C/J]TTAGAAAGGGCATTTCAAGCACATTTCAATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGAGGGTATGGACCAAAAGTGCCCAAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAAC[J/T]GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACTTAGAAAAGGGCATTTCAAGCACATTTCAATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGAGGGTATGGACCAAAAGTGCCCAAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCTTGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCAGCATAACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCTTGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCAGTACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTGGG[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATAGTGAATGCTGGGCTGCTCTCCCTTCCAGGAATGCTGGCCCCAGCCTGGCCA GACAAGAAGACTGTGAGGAAGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAGATCCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTTCTGCTGTCCACAGTGAACACAGCACCCAGGTGGCCAGGGTCCGGCTCCACACA[G/T] CCCTCAGCCCCCTTCAGCTTTGCAATGCTGCCATCGGTACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCCTCTCCTCGGATTTGGATCTAGCAAGACCAGACGGTCTCTAGAA TCCTGACTGTTAACAAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTTCTGCTGTCCACAGTGAACACAGCACCCAGGTGGCCAGGGTCCGGCTCCACACA[C/T]AG CCCTCAGCCCCCTTCAGCTTTGCAATGCTGCCATCGGTACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCCTCTCCTCGGATTTGGATCTAGCAAGACCAGACGGTCTCTAGAA TCCTGACTGTTAACAAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAGTGAAGTACGGTGACCT GTGAGCCCCCATTCCT[G/A]TGGGATAAGGTGTCATTTGTTCTTGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAGTGAAGTACGGTGAC CCTGTGAGCCCCATTCCTCTGTGGGATAAGGTGTCATTTGTTCTTGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGTGAAGTGAAGTGAAGTGAAGTGA CCTGTGAGCCCCATTCCTCTGTGGGATAAGGTGTCATTTGTTCTTGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTGTAAATGCTTGGTTATTGACTCCAAAAATTGAATAAGTATTGGGAAGAAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTGAAT TTCATATACCTCCATTATTAATTCATATCATCTGTCAGAGAGAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTGTAAATGCTTGGTTATTGACTCCAAAAATTGAATAAGTATTGGGAAGAAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCT GAATTCATATACCTCCATTATTAATTCATATCATCTGTCAGAGAGAAAGACAAACGGTGCCAACTG GGTTTGGTGGTGCCTGCACACCCACAGTGGCAACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---			---	ATTGTATGCCAAATCATAATACCCCTGCACTTCTAGAAACATACAGTGTATAGAAATTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTACGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGTA/CIGCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTGGGACTTAGGATGTAG
WI-10613a	44 G A ---			---	ATTGTATGCCAAATCATAATACCCCTGCACTTCTAGAAACATACAGTGTATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTGGGACTTAGGATGTAG
WI-7587c	133 A T ---			---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA/AV TJGGAATGAACCACTCCCTGCCATTTCCCTATAAGAAATATCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCTCATATGCTGAGCCAACTGCACTGGGGCTGCCCTC
WI-7587b	81 G A ---			---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGA ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTTCCCTATAAGAAATATCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCTCATATGCTGAGCCAACTGCACTGGGGCTGCCCTC
WI-7587a	28 C T ---			---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGA AGCATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTTCCCTATAAGAAATATCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCTCATATGCTGAGCCAACTGCACTGGGGCTGCCCTC
WI-10681b	103 T A ---			---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTAGCTTACGCAAACTCAATCAGCCAAAC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC/T/AAAGACAGCCATTTTAACTCTAAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGTGACGCTCTGTAAAAG
WI-10681a	41 A T ---			---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTAGCTTACGCAAACTCAATCAGCCAA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTCTAAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGTGACGCTCTGTAAAAG
WI-7222c	126 G T ---			---	GCCTCTCCTCAACTGCTCGACCCCAAGGCTAGGAAAGGCTGCTGAGATGACTGTGGTCCCTCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACTCCCTGTTCTCAAGTTGGGGATGGG/G/TAATAA AGGAGGGGAATCCCTTGAACAAGAAAGAACTGGGGATGTTATATTTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTGTTTCAAGAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	---	GCCTCTCCTCAACTGCTGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGGAATAAGG AGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCCTCAACTGCTGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/TTATCTCTCTCCAGTTCAAAATG CTTGCACTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGGTACAGAGAACTCTTGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/TTATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGGTACAGAG[GT/TAATCTCTTGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/TTATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAG[TC/TTTAGCCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGGTACAGAGAACTCTTGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/TTATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[CA/GJA CAATCTCTTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGGTACAGAGAACTCTTGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAAACTTCCCTGGCCCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGCTGGTAAGTTAT ACGGTGTCGAGGCAACA[G/TTGGAGAGGTACGGGAATAGTTTACTTCTGTTTTTATTCTTG TG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---	---	TTCCACAAAAACTTCCCTGGCCCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[CA/TTGAAGACGATAGTTAACGCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTTACTTCTGTTTTTATTCTTG TG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127 G A ---			---	AATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCATTTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTTGACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G]A[GCCTT CAAAGCCAAAATAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125 A T ---			---	AATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCATTTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTTGACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G]G[CCTTC AAAGCCAAAATAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGTTTT	TTGTTTGTGT	AAACGTAAAA	TGACATTATAT GAAATGT	CGGACACGTGATATACAAATACAGATCGTAIGGGTTTGTGTGGGTTTTTTTTTT[G]TTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G AG	AACTGCAAAAT AGGAAACCCAG	CCACCTGGGGC TCCC		TTCAGTAAGTCAATAGGAAACCCAGAG[G]GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGTGGCCCTACACCCCTTTAT
WI-8170b	259 G A ---			---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGAGAGATTACAAAGTTAAGATCATGTGTCATCAAAAGTCAATCCTATCAATCAGAA ATAAAGTTAAAGGGCCCTCAATGAAATCTACGGAACAAACATAACACAAGA
WI-8170a	204 T A ---	CCTTTATTAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT		GCACCTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGAGAGATTACAAAGTTAAGATCATGTGTCATCAAAAGTCAATCCTATCAATCAGAA ATTA/AAAGGTAAAGGGCCCTCAATGAAATCTACGGAACAAACATAACAC
WI-8172	136 C G GACA	TGAAATAAAA ACAAATTTCTGT	AAAGGTAC TGTTGTTGAAAT		CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTCAATGGTGAAGAGTCACTGTTAAACACGAA ATCTAACCATTAACCAAGCTTTTAAATCCTTCGGTAACCTCCTTTATTAATAATGTTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCCTTTACA
WI-8183	56 G A TGC		CAAACTGC		AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAACAAATTTCTGTGTC[G]A[GCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATG
WI-14149	83 C T ---			---	GCCTTATTGGGATTGCAAGGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTTGCCGGAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC		TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G]A[GAGATGGTCAGGCTTCTG TTCTTAACCCAGCAGAGCCCCAGCAACCTAGAGGGCCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TOCCCTGGGAG TCTACTAIGG	GGGATTAGGAT TTTAGTGTCA C	GGTGTCCCTGGGAGACTATGG[C/][A]GTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTCTTTAGTCCCTCTTATCCACCCAGCTTCT
WI-8833	51 A T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTTAAAGCTCTGTAGACTGTCTTCCATGCCATTCTCTG[A/][T]GCCCTCTATAATGT GTGAGGTATTACAATAGTCCCTATTCAAAGTCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTTGGTAAAGTTCAATTTTCAGTACATGGGTAACACCCAGGCCCTTCCC[A/G]T TATATCCAGGTATGCTACAAGTCTTTTAACTCTTATCAGAAAGTTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAAATTCACCTTAGTTTGGTTTGCTAATGTCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCTGGCTGTTGGCTCTGCGCTTGCTGTTTGGTTTCTT TCTCTTACTGGTCTTCTTTGCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG TAGGATA	AGTCTTCCCTGA GCCTTCCAT	ACTTTTCTGAGCTGAGCAACCTCATCATCTTTAGTCTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA[C/][T]ATGGAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTATGGTGAACA[A/G]JACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGT[C/][C]GGTGAACAACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAA
WI-8895	32 A C	---	---	GTGCCACAACCTGGACACCAACCAACAGAAT[C/][C]TCCCGTCCCTTTGAAATTTCCATTAAAGACA CAATGGGGTAATTATACAGGGATGCTCCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCTGCGTCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATG[A/][T]GTATCAGTGCATATTCTATGG AAAAATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAG[C/][G]TCCCTCTCTGCCGTTGTACCCACATCCACAGAGCA GCOCTAGTGCAGGTGACGCAGTGCACCCACCGGCACAGGGAACAGGACCCATGCTGC

WI-12108	40	C T A T A	TGAAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[T]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
WI-5989	29	G A CACAGGCA	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGITTAAC[T]GCCCTCCATCTTTTCTTGGGTGAGGACACG
WI-12201	61	C T OCTGCATG	CCCACTGATCA OCTGCATG	CCGACCACATA OCTGGC	ATAGCTTTTAGCCTTTTCTCTGGAGTGTTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGGTGGGGTGATGGACGTGGGTTTGACGCCCTCCACTGCTOGATAAAAGGC
WI-12018	31	A T TCTGACTT	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGAGGCAGCCTCTGACTT[A/T]CTCTCTGTTCTGTCTCTCTCCCCACATACCA ACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATAGGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G CCTC	TGGCCTCGCTG CCTC	AGGGATCAA GAGAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAAGAAACCCTGGCCTCGCTGCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T CATGCCCTTTA AGGATTAAGT	CATGCCCTTTA AGGATTAAGT	TCCTTTCTCTT TGGTAGTGG	AGCATGAAGGAGCAGTTTTATTGATTGGTATATTCAAGTTTCTAACCCAGCTGAAAAATTCAATA CATGCCCTTTAAGGATTAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C AATT	GTTGAGTATTT GTTCTGCTCAT	GGGAGGCTG GTACATATTGG	TCTGATGCTATTTATTGGCACAAAAATTTATCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTCATTTAGTTGAGTATTTGTTCTGCTCATAAATTT[C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G A CA	GACAGACTTC AAAAGCAATT	AGGTTTGAANA TATGTATTAAG TACTTTGT	CTGACAGACTTTCAAAGCAATTCA[C/G]CTTCCAGAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	TTAAATCCACACTGAAGATCTGGAGTATGGGGGATATAGGAATTTGAGCATATGTATTAT[C/T] TGAACATAAATTTACAAAAGTGGACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTACC ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCACGGGAGGTGCGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11305	87	C T ATCACACCA	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATTTTATATGAAGTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAAATTTTTTAA A/GJAAAGTTTAGCTATCCCCAATGCTATTTAATACAAATTGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11321	67	A G TTTT	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTTGCC
WI-11324	40	C G GTGCCCCA	GGATAAATCA GTGCCCCA	ATCAAGCTTTG GGGCTCT	

WI-11352a	69	T C G	AGCAGCAGC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGATCATCTACATAAGCAGCAGCAGCATAGTGGAA AGTTCGCTAAGTGCTCTACGAGAGGTCAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACITTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCGCGGCTGA GCAC	TTAGCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTACGTCGTGCTCAGCGGGGCTGGACATCCATGTTTGGAAAGAGTTGGCGGGGT GATTTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTGGCTGATGGTGACACAGAGACTTTCATATCTTGTGTTTTTAAAGTC TCTTCAGTCAGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAGAAATCAGC
WI-11388	88	C A A G T T C	TGTTGAAAT ACACGTAAC AAGTTC	TGCCTTGATC CAAGTTAAAT T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C/A]TATAATTTTAACTTGGATACAAGGCATTTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGAACITTA	GTACATTCAG TGTTTTGTAA AAG	TTCATCATTCCTCAATTAATAATGGGAGGTTATGTGTTCTTGAACCTTAATAAATAC[T/G]CTTTTACA AAACAGTGAATGTACTTTTCTGTGCAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTC ATATTCACTCA TC	AAAGAATAAGATGGCATTGTTCAGTTAATTTTGTGTTTTGAAATGGTGTGTTTATGATGGGTGAATA TGAAAATAAGCTTACCTCATCCACTCTAAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCACCAAC CAGC	TGCCAGGGCT TATTTG	CTGTCAGTCTTCCCAACTAAACCGTGAGTTCAGTATGTCTGGCAGCAGCTGCTGCTGTTCTGGTG TATTCOCATTACTGAATCCCAACCAACAGC[C/A]CAATAAGGCCCTGGCACAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T T A T T T G C A	TGAGAAGCCA	GTTTATTGTTA TAAAAATGAC CTACAACIT	ACTTTGAGAAGCCATTTATTTTGCAG[C/T]CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGTGATTTTATAACAATAAACTTTCTATTATCTATTATCTCTCACATACATTT CATGATCCTG
WI-13364	35	A G	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A C A G A C	GCAGCCAGG AGCAGAC	TGTAAGGGA GCGGTG	AGGCAACACTGCTTTATTAGCGCGGAGCCAGGAGCAGAC[A/G]CACCCGGCTCCTCAGTACACATT CCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGGATGGAGGGGCGAGCTAGGCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTGC ATATGTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCAT[A/G]GGGAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	AATGGCTGTTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTAGTTCATTACATG[A/G]TACAAATCATTAGAGICTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	CT A	GGTCATTGAT GGAAAGACAC	AACAAACCA CCTGTAATTT GTAAC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G GTGGGCTT	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTCTTAAACTTGAGCTTGCAGAGAACACTTGTGGGCTT[A] GTTCAACATGAGCTGATAGTCCACCCAGATTCTAACTGGTAGGCTGGGGTG
WI-12345	37	CA AAAGAGAA	GTGGCAGAA AAAGAGAA	TTCAGAGGGG TTCAGG	GGAAACAGACCTGATCCACGTGGCAGGAAAGAGGA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTTGACCAGCTGGGCTTGGCACCTTTGTGAGATTTGCAAAA
WI-13416	71	CA AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTATTTTCAAAATTTTGGAAAGTTTTTCAAAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTAATTCATTGAACTATAAACACTTAGCAGAGGAAGGGACTTTTGAT
WI-12310	46	GA AAAAGC	TATTCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGGTCT AAA	TTTGAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAGGCAATTTTCTTAAGCAG T
WI-12086	72	CT TTGGATTT	CCGGGAAAC TTGGATTT	GGAGTCTGG GTCITGG	GAACCGAGCTTTATTGGAGCAAGAGGTGGACACTGTTTACAACAAAACGTTTCCGGGAAAACCTTG GATTT[C/T]CCAAGACCCGAAGACTCTCCAAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGOCCTAGCT
WI-11549	102	T G TTTTATG	GGCATAAAGT TCATAATATTTC	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTAATTTTGTAAAGAGTTTGCTATCTAAATTTTCATAATTTATTTGGCATAAAGT TCATAATATTCTTTATGATCTTTTAAATATCTG[T/G]GGGATTTGTACAGACTTTCTCTC
WI-11585	79	T C AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTCC	TTAGAGGAAAGAAATAAACACCGTAAATGGGAAATCAGTTTCAAGAGGTAGGAAGGAGCTGGGT TGCAAAAACAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGAGCGGGTAGAGT TT
WI-11604	68	GC ...		---	TTAGTTGGTTCTGAAACITTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGAGCTTTTCCATGAAATAATTAAGAGCTAAGGAATTCIGACGCTCACCATTCTTC TTTGTTACTCTGCAGTT
WI-11614c	108	CA ...		---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAATAATCCAGAAAGCTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCAGTGTGAAACTGCA[C/A]ATATTAAGTATTCGTGAGCTAG GGACTTCGT
WI-11614a	60	A G CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGTGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAATAATCCAGAAAGCTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTGAGCTAC GGACTTCGT
WI-11626b	83	T C ...		---	TTGATTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGGTACAGGATAATATACTCAG ATATTTTAAAAATAAAT[C/T]ACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAATTAATTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCTTCCCTCC CATGTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTCCATTGTCTCT[C/C]CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCCGATGCAAGTCCATCCATG
WI-11636	61	A G T C C T	GGACTTAAAA AGATCTGCTTA	AGAAACTTGCT AAATATTTTAT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
WI-11637	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCATT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGAOC
WI-11654	37	G C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCTCCAAAAGACTATTAGCAACTG[C/G]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTTCATCTACTCAGAGTTCACACTCATATTTTCATATTTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAACGTC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTACTTGAGGACAAAAGCCTTGCCCTGCAGTTGTTT AAAATGTCCTGAAACAATCAGATTCACGCTGGAT
WI-11680	55	T C	---	---	ACAGATACTTTCCACGGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[C/T]TGCCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAGATACCTTTGACATCTTATCACAGCAGGGGACAGT[C/A]AGGTTGGCTTCTCTA ATGCCCAACATCTTGTTTTCAGAACTCTTCCACTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACCTTTCAATAATTAATAATCGAATAATACTGAAATAACCCACAGC AG[C/T]TTTTCAGTATAATTTTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGTCAGA
WI-11706	60	C T	TGGCTGGAATT TTCCTCTCT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTCTGTACAATTTATTTGG[C/T]GGCTG GAATTTGTTCTTTGGGATTTGCCCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTACGGG A	AATATCATCACTCATATCAGGATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGCTT[A/G]TCCCCGTAAATTAGAAGAAATGAAT GGCCAGATGGATGGAATA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACACAGCCAGCCCCACACTCTAGACAGCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCA[C/A]CTCCTCCCTCCTCCACACTCCTTC

WI-11715b	123 C T	AGCTGGCTGC AGCTT	TCCCATCTCG TGCCCT	AGAATGGAGCTGTTGGGGAGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAGAAAGGCTGGCTGCAGCTTC/TJAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C AAA	GCACACAATG TAAACACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGAGACATGCACACAATGTAAACAGACAAA/A/CJTGCATTACAACCTG TGGTGTAAATGTGGCCACTATGAATCCCTATGTATAAGAGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C TCAACA	AACAATCCTT AAAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAAATCCTTAAACAACTATCAACA/G/CJCTGCAACACAACACAGGC AAATGAAAACAGATGCCCCAGACAGCACCCACACATGGCACACAC TTTTATTATCAAACTC/G/CAATTCCTATTACAAAATGTAAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTCTTATCTCTTCCCAACCTACACTTCTCTCCCTACAAACCGGGTCCAAA
WI-11728	16 C G ---	ATCTGTGGTTT TCTGCTG	--- TGATTGGCCT GTGGTCTA	TTTTCTCTTTTATTAAGTCGCTATACTAACTAGAAAGGAGAACTGTGGTTTTCGCCTG/A/GJTAG ACACAGGGCCCAATCACAGCTTCTGTAGAGAACTGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G AATATAA	GCCTCACAAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAACTC T	CCGGCCTCACAAAGTATTTTCTAAAAATATAATTTGCTA/GJTAGAGTTACAGATGAGCAGCTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT AGCATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAACAGCAGATCAGAGATTAAAGAAAT ATTATTGGCTCTTTTCTCCCTC/GJGTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11773	93 T C ---	GGCTCAGAGA GCAAGGGAA	--- GTTG	CATGACAACCTCTTTATTAAATGGGCTCAGAGAGCAAGGAA/C/GJACACAAAAATTTACAGTCTGA GTTTGGCGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTATACACACAGACTGTCCAAGCCTC AGA
WI-11282	42 C G	CCCAACTTACC AAACCTCTG	CGGTAGCGAG GCTAAGC	TAATTCACCAACTTACCAAACTCTGT/GJGCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGCAAAATCATCTAACAAAAAG
WI-11790	28 A G	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACITTT	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/AJAGT GATTTCTCTCTTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-11879	61 C A AGTATACA	GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTCCCAITTCCTCCCTTTTATAGTTTTAATGTGGTATTAGAAAAGTTTAAATACAT ATGTGGCTTATCTTATTTCTA/C/JTGTGACAGCAGAGTCTTCAAAGTTTGTCTATAGACAATCTGA AAATGGGTTCTGAACT
WI-12489b	91 C T AAGTTTAAA	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/GJTGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATCTCAGAATGCCAGAGTAAGATGAACCCCTTACAG
WI-11906	52 A G ATCTGAA			

WI-11909	78 A G	TTTGTTGGG IGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAGACACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTGTGTTG GGTGGTCAAG[A/G]CTATTAGAAAATCTCAGAGGAGGACAAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGCGAGTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAAGTACAACTGCTTATTTTCTTGGTTGAAGATCAGATCTCTGGTTTATTTAA[T/ G]ATCAACATTCCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAAGTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAA[T/A]AATAAAAAATCTGTAAACATTTCTCTATTTCTTACGA ATACTTCTTTTGTATTTGCAATTTCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGTACCTTT GTGTTATTTCTGTTTCACTAAGGA[C/T]AGACTTCAGAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA TAC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAAAGTTCTCACTCTGCACATATAAAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCAAAGTA C[C/T]GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110 G T	CAGAAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTTTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGGGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAAGCTACAGTAATTGAATACATGACCAATTT[C/CTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A ---				CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGATGTACATACCCAGAGCAGGAGAGAG AAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTAT
WI-11076a	106 T C AGGCA	AAGGGGGAGC	TCCTGCTCTGG GTATGIGAC	---	CATGGTTCTGCGAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGATGTACATACCCAGAGCAGGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTAT
WI-14263	49 T C GGCATATTCA	CGCAGAAAAA	GGTTATTCAAA AATTAGTATGG GACA		ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAT[C/T]GTCTCCCATATAATT TTTGAATAACCTAACTCTCCCTTTTGTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGAGCAT[C/T]GAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28 T C ---	CTTTTCATTTT TGCTTTTAA	---		GATTTGTTTATTCTCGCTTTTCATTTTGGCTTTTAAATAGAACAC[G/A]CTTTTGATTTTGTAGTA TATGACATCATCATGAAATTTTCTCTACTTTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50 G A TAGAAC	CATGAGAGGA	ATCAAAAG		ACCTCTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGCTCTACTTTTGC TACAAATCAGGATGCAGGGCATGAGAGGATTCCCTCTCTG[C/G]TCCAAAGGAAAGCTTTTGGC AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTTCTTGTAAATCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGTGCTG
WI-13951b	88 G C ---	GGAGTGAACA AAGTAATGAA	---		G AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCGAGATCAGAGGAAGAG ATGGCTTTCTTGTAAATTTCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGTGCTG
WI-13951a	39 C T CAAAA	AAAAAGGCTC	TTCTCTGATC TGGGGTCT	G	GAGACCAAAAAAGGCTCTTGCCCAT[G/A]ATTCCCGTCTCTCCCTCTGATGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGATGATCCCTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAG	GGAGGGAGAG ACGGGAATA		TTATTTGTCAATTAGCAAAAGGAGTTAAATACTGATAG[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAATCTGTTCACTGTCATTTCCCTCACAAGGAGTTGAGCCCTTAGATGAC
WI-13960	39 A C TGATAGA	ATCTTATAACC AAGAGGCTT	CATGAAAGGA CAAAATTTGCAT C		AACCTTTTATTGTTTAGCTAGCCCCAGTGACTTTTATGCATCTTATAACCAAGAACCTTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTTGCTCAGGGTCCACAGGAACCGGCTTTGGCT
WI-15843	62 C T CAG	ATCTTATAACC AAGAGGCTT	CTCTGGCTCAG ACTTGCCT		

WI-13983	52	G A	TCTCCCACT CCTTAAACCT	CAATACCTCT TAGCCAGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCTTGA/JCCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACTCACTGACTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCATG/JJTACAAAACATTGT CAGGGAACATTTACAGAAATAAATAAGATGGACTTGCAGGTGTAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGATG/CJTITTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGAAAAATATGAGTGAGACTCA
WI-14284	55	C T	---	---	ATTTCAAAACAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAAACA/CJTJATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGGCTCCCTGATGCAITGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAATCTT	ATGACCAGACCAGAACGCCCTGTTCTATATGAAGACAAACAGGTGCCCATACTTTGGGTGGAGGGATA CCGCTGCTATTCCTCAGATG/CJJAAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAAC/CJTJGAGAACCACTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCATACACTT CTCACTCTCT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCA/CJTJAGCAAGAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A	---	---	TTTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTATG/AJACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAAGGATACAGAAAAAACTCAGCGAAGT/CJGAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC/G/AJAACCTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTCCTTTGACGCGCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAACCAAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGAG/JGJCATTTGTTTTTATTAGCTTGTCTTCAAA/JGJGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGGAG/JGJCATTTGTTTTTATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTCACATTC AGAAACATTTT	CTGACTTTATTTAGCATGCAATGCAATTTATCTGGCAATAAATTAATATGTGCAAGTTATAAAAAAT GTTGGGTACTTTTTCCAAAGATJAAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAAAATCAACA TGTGCACAAAAAGAGTAAAAATJGACCAAAAAATTAAGATTTTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCCCTACTGGACCAATGCAATCTAGAGACTGGGA[C]ATGGAATCTAACTGCGCAGAG AAATCAAGAGACCGATGGTGAAATCTGGGGCAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAC CCAAATTTTTCATTATTGCC
WI-13857	28 A G ---		---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAAATGT CTGCCCATTTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTAAAGTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCCJTGJTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---		---	TTAATCAGTCTGTGTCAAGAAGAAACAGGACTTGATCAAGCTCCAGCCCTCACCACCTATATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAGGAAJATJGGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTTCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCTACTCCACTCTA GCTGCAGTAAATACJTGJGCATCCCATCCACTCTCTCTCTTTTGTACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATTTCCAAAGATGGGAAGCG[A/C]CATTTTTTCATTGGCTTGAATGAGAAAGCTTCTACTCCACT GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGCTGGACACTGCAGTGAJTCJAGGG GCAGGTGTGGGGCAGGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCCACACCTGC CCCT	TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT[A]JAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATAATTTGCTTTTCCCGAGGGCAAAAAAGA GAGCTTCCCAGAAACCTC
WI-13578	48 T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACCTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCCTCCTCTT GAGTCCCT
WI-13789	62 G A	TGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGCCA GTACTTTT	AATAACAAGTTTAAAGTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGCJ GATJTGACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAAAACAGCTGC

WI-15625	40 C T	---	---	GTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGTCCTCCATAATTTTGAATAA CCTAACTCTOOCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCAG	TOCCACCCGA COCT	GTCTCAGTTTCTGTAGGCTGTAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATAATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC	CATATTGAAAA TTGTTACTAGA TGATGG	CTCAGTTTAAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTAGGGAAGAGATAGAGGACCACCATCAGCAACCCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAAACACA	GCATACCTCAT GACAAATATTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCOCA
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTCAACAATTTTCAC TTTTAAAAAC[A/T]TAAAAAACTACTCTTCATATCCTAGCCCTGATGACTTAAAAAGTTACCGG
WI-14319	83 C T A	CAATTCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G A A A A	CAATACATTT GCATTTCTCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCAATTTTCTTAAAA AAAGAAAGACATTT[A/G]TTCAGAGAAAACTGGTATCATCGAGGAAAGCAGAAAAAAATTT
WI-13909c	93 A T	---	---	ACTTAAACTGGCTTATCTTACCGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACCTCGAATATCTTTTTC[A/T]GAGATGTCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTACCGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACCTG[A/A]AATCTTTTTCAGAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	---	---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTTAAACAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCATTTCTGGAC[C/A]ATGGGAACCTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTTAAACAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCATTTCTGGACCATGGGAACCTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104 G A A A A	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTGGGAAGACTACCATTTTCAAAATTTATTATGT AATACACTCATCCAGATAATGAAACATCTGCGAAAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGCTTCCA AA	AAAAATGACAAATCAACTAGCTTGGCTTTTGTGTCG/AJTTTGGAAAGACTACCAATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTCGGAAAAGAGTGGGAATCAACCTCATCTGTGC
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATGCTTCAT TTTAAACTAATTTAGTGTTTTCJTTTAAATATATGAACCTTTTGGTGAATTTATGAACGTGTACCAAAC C
WI-13752b	117 C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACCTGCGAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGCACGTCJGGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106 T C AGTGCTGA	CCCTCTCGTTA AGTGCTGA	CCCTCCGTAA AGGTGTC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACCTGCGAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTCJGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102 T G TTAC	CCCAATCAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACACCCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCAACCAATCAACACAGTACATGATTACJTGCGGTTCCAGAAATCTGGATAC
WI-13744	115 C T AAAACTGAA	TGGTGCTGAAC	AATCAGGAAA GATAAGCACA GC	TGGATGATGGATGAGGCCACCTGTGTTCAACAAAACACAGTAAATGGAACTTCATGCAGCTTTAGAT TTCCCTTGCCAGCTAGGAGCTTGTGTATGGTCTGAACAAAACCTGAAJCTJGCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T ---		---	CCCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAAGAGAGCCCCCGGTACATACCTTAT JCTJAACCAATTCATCCACCATTGTGTAATAATCTCATCTTCTGGGCTGGATACCTCAAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACCACTACCACTGAATATATACTGAATTAACCTTCAACCCCTTTCATCCATTGAG CJACJAAATTTAAAACCTCTTGCCAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATACATAGATCAAAACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTTGGTTCTCTAAATCGATACATCCAAAACCTTTCJAGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T CACA	ATTTTATTCAC ATTAAACTTG	GTCTTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAAACTTGCACAIGJTTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGGAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGCJGJTAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAAATGCAGCAGCAGGAGATGTGAAGACJACJCAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG

WI-13785b	40	C G ---	---	---	TCAAAAGTGCACACTATAAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27	T C TGCTT	TTGTTGACAG CTATGTGTAC T	TTGTTGACAG CTATGTGTAC T	TCAAAAGTGCACACTATAAAAAGTGCCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88	C G ATAGG	GGGAGGAGGA TTTGTTACT	GGGAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAATAAAAATAGTTTTACCCCATTTGATACAACATAAGGGATTTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAATCTATGACTTG
WI-13794	52	A G TTCTTTCTC	AGAATGGGCTC TTAACCTTGT	AGAATGGGCTC TTAACCTTGT	TAGTCTCCTACAAATCCTTCAATCCATTTCTTCCCTCACCCCTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCAATCTTCAACAAACAAACAAACATAGAGCAAT
WI-15729	35	A G GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/G]GGCACCTTTAGAAAGAAAGCTGAGACTGAA AAGTGTGCTTGACTTCCAAAGGAAGGTAAAGTCCCTGTTTGCAGCCCGGGCCCTGCTCATTGTTA
WI-13424	66	G A C	TGAGGTTTTTC ACCTATTCTT	TTTTCTCCCC AGGGTCTA	GTCCTTTGACAAAGTCTCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTACCCCTATTCTTCTC[G/A] JTAGACCTGGGGAGAAACACATGTGTAAAGTGCTCAGGACATGAGGCAGGCCGCTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T C AAT	CAAGCTGAATC TGGGATCTC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGGCAATTT[C/G]AGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCCTGAACATCTTGAAGCACGAA
WI-13446	22	G C TCACTCATCA	AAGGGAATCA AAATCAGAAG G	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCA[C/G]CCTTCTGATTTTGATTCCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTAGAAATCTCGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56	A C TGGGTGOC	CCTGCTGTCTC GGGC	CCTGCTGTCTC GGGC	TCACACAAAGGCAATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/A/C]GCCCGAG ACAGCAGGATAAGTTTACAAACCTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTACAGGATG
WI-15702d	107	T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCTGTAAACAACTACTAA[C/J]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A A G	A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A A G A G A C C C G A C A A A A T A A A G G C T T T C A A A A G [G/C] G G G T A A A G G G T G A G G A A G C A T G T G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A T A G T T T T G A
WI-13831b	113 T C		---	T T T T T T T A T G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T C C A C T G T A T C C T C C G G T A A G T T T C C T T C T C T T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C		---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-13806	62 G A		---	C A C A T T T C A G C A A C A A A T C G A G G T G C A A C A G G G T T A T T C A C A T T A A T A T A T T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T T A A A T A A C C A T C T C C T C A C T T C A T G C C A G T
WI-14372	86 A G		---	A G G C T G T T T T G A G G C C T G A G G A C C C A A C A T G A C A C G T A A G A C T G T A A C C A T G T A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T C A C A G C C T C T G C A
WI-14373	95 A G	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T A A A C T A C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A G A A A A	C A T T A T T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T A T T T C A T G T G T A A G A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T T C T T	G G G T C T G A G G T G A A A G A A A A A	G T C A A A G G T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T C A T T C T A A A T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T C C A T A T T T C T T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A G A A T G A A G G A G G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T A T T G A C G A C T A C A G C T C C T C T C T T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G G A A A T C C T C A T C T G C G G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CAAC	ATCATCTGTT TGAGGTGACA ---	TTTATGCTGTTGTTTCTACTGGTGGTCTGGCTCACTAATATCAATCCTAGTATGATTTCTTT TACTTGIGTCTATTACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGAGAAA[C/A]CCCACTTAAAGAGGACACTGCAGAGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	---	---	ACCGCAGAGCTGCTGTATTTAAA[A/V]JACAAGCGTCTGGATCTCTGCAGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCAOCCC
WI-15937	24 A G A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTTTCTCTCA[A/C]JACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGAAAAGGAAGTTTCAGGTGATACAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A	AAACTGAAAC GTATTTCTCC	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G	---	---	GACAAAGAGGAGCTTTCTGTAGTCCAGCGGCCAGAGCAGTATCAGAACGGTGGTTTGACCT GCATAGATTTTGTGACGACT[C/T]GTGGCCATGCCATTCTGTAGTGAAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GCCAC	GTTTATTTCTCACAGTCTGGAGTTAGAACTGAGATGAGGATATCAGCAGCATGTTAGGTTCT GGTGAGGAGCTCTGGCTTACAGCTGGCTGTTCTCACCATGTTTCAAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14136	120 G A	GCCTTCTCACC ATGCTTTCACA	CTTGTTCTGTC TCTTTGGGC	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23 C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTTCAAACTTGGAAAGCAACCAAGATGTCTTCAGTAGTATATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCAATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	GACAATC	TAATATT	TTTTTAAAGAGTGCTTCACATCATTTATGTTATGTCACACAAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCCTTCTTCAGAAATCA OCTOCC
WI-15953b	59 C T	---	---	TTTTTAAAGAGTGCTTCACATCATTTGTTATGTTATGTCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCCTTCTTCAGAAATCA OCTOCC
WI-15953a	26 T G A T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG A	TTTTTAAAGAGTGCTTCACATCATTTGTTATGTTATGTCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCCTTCTTCAGAAATCA OCTOCC

WI-14631	82	G A ---	---	---	TGAATCAATGGACAGTTTGCCTCTGTTTAGTGAACCCCTCACAAGCACTCTGCATAGTCGCTTT CTGTCTCTTTAAAC[G/A]TGCTGGTTCCTCTGCCAAACTTTTAGGATTGGCCCTCTCTCAGGGCCTT GTCTGA
WI-6053	24	A G ---	---	---	ATCACCACCGTGTCTAAGAACAAC[A/G]CTTCTCATGTCCAACATCATCCCCGGGACTTTGTCAACTG CAGTACACTTCTGCAATTGAACCTGGCTTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGTGC AGCAGTGAAGGGGTATATCTGGGCTGGCCAGTTGGAACACGGAG
WI-15964	99	T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC	---	CAGAACTCTTCTGTGTTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGCGAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGT[A/G]GCAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG TCTTCTCTTC	---	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAGGGGAGGAG CCT
WI-12179	96	G A TGGAGGTCA	TCGAATGACCC TGTAGATGC	---	TAATTTAAAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTCTCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	CAAGAATCAT TCTCATTTAAA	---	CACAAATAGTGAATATCTGAGCAAGAATCATCTCATTTAAAAATTGTC[G/A]AAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAAAATGACACTCCCAATTTTACAGGTAACTGTTA
WI-14666	105	T A ---	---	---	AATGGGACTTTCAACAAGGGTTTAAACTAATCTAATAACAACCTCTACAACAACATTCAGAGCAT TATAACAAGAATTATTTACAGGCAGCTAATGTATTAAAT[A/A]AACCATGAAAAAGAAAAAACTTG ATCTAGATGTCAGCAATGGGCTGAGACTGTC[T/G]GCTGAGTAGTGCAGTGTGTTGTATGTTCTTAC TCTATTACAAAAATTACAGAAATATGGCTTCGCTTTTGCAAAATGTTTATATACAGTC
WI-13967	103	A C AAATAAAAA	AAAAGACTAC AGATACAAGG TG	---	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAAAGATAAAATATGTCATTTCAGCAGTCATTT AAAAAATAAAGACTACAGATACAAGGAAATAAAAA[A/C]CACTTTAGGAGATGAAAAACACAAA
WI-14408	60	T A G	GCAGACACAC TATTACAGGCT	---	TTAATATTTGACGAAAGTTATTGCAACAGGTTGAAAAATGCAGACACACTATTACAGGCTG[T/A]AA GTAACAAATGAGTTTACACAATTAATAATTAAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C G ---	---	---	TTTGTGTTAAGAACAGCATTTTGAATAAACCCTATCTGCCCATG[C/G]TTTACAGCCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGIC
WI-13910b	63	C T CGTCT	CACCATGGCA CAC	---	TTAGAAAACTGATAAAAGCAACAACACTTTTGGGAAAGCACCATTGGCAGCTCCTTTGTGCTA[C/T] GTGATAAGTGTCCTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---	---	ACATGGAGATACAGAGCTGTC[G/A]TCTTGAAGACCACCACCTGACCAGGAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTTGACCGTCTGGGAGCGTTGAAGGGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59 T	GATAACATAA AATGATCATG C AGAATTC	GCATCTCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC	AAAGTAAAG CTTTGTGCCTA AAA	GTGGAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCACTTGAACCTCAAGTCATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA
WI-14759	73 T C	GGGTTTGACTT GTGGGG	TCCACACTGC OCCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATTTGGTTTTATTCAAACCTTCTAGCGTTTGACTT GTGCGGT[C/G]GTACTCAAATGGGGGCGAGTGTGGGACGGGAGGATTCACACAGATTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[AT]CTTCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCCC
WI-13805a	112 G A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAGGAAATTTTGGC COCAGAAACCATGAGATTTTGGTGCAGAAAAAGGCACACGGGGA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	---	---	ACACAATAATTCATT[C/G]CGAGTGATTAAACCTATTGTTGTTAGAACCAACAAAACTAC AAGAAAAACATTTTCAAACCTTTTTTTTTCAGGCTGA
WI-14808	52 T A	ACCACACACA CTACCTGT	GAGGATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACACAGTTAAAAAGTACCCACACACTACCTGTTT/AJAAAACTTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACACTGAAGGCCCATGTA AGTTAAAAAAATCGAGTCAGCATTTTATTA/TAJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-14816	29 A T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTTAGAAAACTGGGATACAGCAGTAAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATTTCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TC TTG GAGG GATAGAGGACAGAGTGTT/CJGTTGATTTTCGTTTCGTTTCAGTTTGGTTGTCATT GGTTTTTGTTTTTGCTAATTTTGCCCCACCCTATAAAAAGCAGTGCACCCACAGGCGAG
WI-14856	60 A T A A	TGGTGACAG GAAAATACCT	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCCTATGATAGCAACAATAAATATGATGGATGGTGACACGGGAAAATACCTAAT/ATTTAA AGTTGTAAAAAGTAGCAACAATAAATTTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAATAATTTGTCAAAAGGGCAAAATATTTTGTCTG/GA/JAG TTAATAAGTTAATAATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGACGACATTCCAAGGCTCTCTAACAT/CJGAGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTATT	ACGGAGTCGTCTCTGATGATTTCTTTGTCAAAAAATGTTTGCCTGATTTCTAATCATGAAAGAACAATT AGAAAAATCCAAATTGACAGATATTCTGCA/GA/JAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/ATC/JAGGTGCCACTAAGGAAA ACTTCTCCAT/CJAAAGCTGCTGTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCGTGTTCTGCTT
WI-14898a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/ATC/JAGGTGCCACTAAGG AAAACCTTCTCCATAAAGCTGCCCTGCTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCCTGTGTTCTGCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/GA/JATTCCCCTTGCAGCAG ACATTTGTGAAGCTGCTGTGGCGCACACCCCATCAATCAGTGAAGTGCCTGCTGACAGAGGGGCGCACATG CACGATGCTCAGGTG
WI-14911	52 G A C	CCAATACATT CAGTTCCCTGGT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTCAGTTCTGCTG/GA/JAAGGTCCCTTTTC CTGGTTTGCAGACAGATACCTTGTCTGTATCCTCACATGGCAGAGAAAGAGAGGAAAGTAATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCCAGCAATTC TAGTGATAGTAGAGGACTCA/CJ/CCTGCACTGACCTTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCCAACCACT
WI-14914	66 G C A	CTGGACACAG TTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCTTGATTGGCTGTCTGTAAGCCCTGTGAAGTCAATGCACATCTGGACACAGTTTCTCTAGCA/G C/JGAATTTATGTCTGGCTGTGATGGCTTTCACAGC
WI-14926	49 T C ---		---	GTTTATTTCAAATGACACATCCAGATTGAAATGGGCACTTAGCGAAT/CJ/ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTCAAAATAAAAAATTTTCCITTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAAAACATATC AAGGAT	TGGAAGAAGATT CCAGCC	GCATCTTTATTACACAGAAACTCATTTATGTCTTAATCATTTGTTTAAATATAATATAAGCATGTT TAACACAAACATATCAAGGAT[C/][GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCTTTTCCACAGGAGGAGTCCCTCATGGAT[C/][GCGGTATTG GTGGTTGTGTGATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA[C/][CTCTAAATCATCTCTTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATACACACAGTACTTTATGGAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACAGACACAATTAAAGGGTCCCAACGAGTTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/][GTTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAATTAAA GGGGTCCAA	GGAAGGCACATA CCAACCTC	ACATTAAACAGACACAATTAAAGGGTCCCA[C/][GAGGTTGGTAGTGCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C	AGGGAACCTG CTAACTTGCA	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTCTTATTGCCGTCTCTCAGGGAACAGGGAAACTGCTAACTTGTCAAGT[C/][CTCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGTCTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTCTACACTTGAC[A/G]GTAATATATACTG TTTTCTGACATCTGTTATCAACTCTCTGAAAATC
WI-14958	83 A G	AATAATTAT CTCTTCTTTT CAAGGG	AATGCATTAT TTGGGTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATCAACTCTAAAATCCAAAGATGAAAATAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAACCCAAATGAATGCATTTTTCAGTTTCTCCAGGCTTTTGAAGTGC AGCAGAAAATCAAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG	TCAAAATAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTGCTTCGTTCAAAG[C/][GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/][T]TATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTITGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTCT	TGATTACATTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATCAAAACACCACCTCTGCATTA AATGAAGCTGCAG[C/][TAGGAAGCTGAGCACATAGCACCCTAAGTATCGGAAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAATGCCTTCTTGA TTTCCCT[A/][TTCAGTTTAGGCTCAAATGGGCTCTCTCCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGCTAAGTA[G/][TGAAGTTTGTGAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACAACTT CATGTACCTAT	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTAAATCTTATCTCTTTTATACACAATACCTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAACAGAGGACTCACACCTGTGCATAGACAGCAC
WI-14683	91	A T A A A C A	AAGGGACGAT TAGTATCTAA	GGCATGTCCA GTGTTTT	CATAAGTTGCATTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAACA/A/TJCAAAAAACACTGGGACATGCCCTGAATTGCAAGT TGGAGTTCGTAAGAACTCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAAATTTAGGCAAGAGAAACAATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTGGAAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/T/AJCTCACAATACCATATACAACATACT TTCAATCACAACCTCAATATAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGGATACCTTTTACTTTGTGTCATTTTATTCTATTG/A/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTTAAATTTAIGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CATTAACTTAC	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA/C/JATTGTAAGTTAATGTAATTTGGCAGCATT GCCAAAAGTTTAAAGGAGACTATTTCTTTAAACAAAAGACAGTGTCTGACATTTATTTTCAGGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGTCTCT	TCAGATTTTAA CATCTCTTTCT	TTTTTTTATTGCAATTTGAGTGTCTTATTATATTGGGAATTCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTGTCTCTCT/C/JTGTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGICCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACACGACAGTAGAACAGTTCCACACCTGATAAATTCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAAATG/AJAATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACITGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTCOCAGTATCATGTAC GCACTAAAAAAAT/CJGTGTGCTGTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A T C G C	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/CJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTT[G/T]TACCT TACTATCTCTAGGCTATTGGAGTGTTCCTCCAC

WI-15100	74	G A	---				TCTATTACAGCCAAAGAAAAATACCCAAATATTTCCAAATAAGCAAAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTCTAGTGGACTTTAT
WI-14492	92	A T	AATTACT			GTCACCATGTT ATATTTCTTT TAAGAC	TGGTACAGAAATGTTTAAATTACAGCAGGCGAGTGATTCAGTTAAATAAAATTTAAACCTTTATTTT CCCAAAATATAAAATTAATAAATTA[A/T]GTCTTAAAGAAATATAACATGGTGACAGCTTT TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCCTCCCTGCTCTAGAGTGGGACAAAAAGTGGGGTGAGAC AG
WI-12002c	89	T C	---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAAGTGGGGTGAGAC AG
WI-12002b	68	G A	---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAAGTGGGGTGAGAC AG
WI-12002a	30	C G	GGACAAA			TGGTTTTGGG TGTTTTCTT	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACACATGGAGACAG TTCTGGAAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAATAATTGCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-15116	96	C T	GTTGCAGTAA			CCTGAATATGC AATTATTTAT ATGACA	GCAAAAGCAAAGCTATGGAGGCTAAAGGAATGGAA[C/T]GTGTTGGTGGTGGCTGATACCTGGT GCTTGTTGCTATGGAGCAGAGTCTTCTGCTCCATGCAGGGGCGTCACATATTTAACTGCACATAAT TTGGCAAACTGTCATTG
WI-12578	37	C T	AATGGGAA			TCAAGCGACCA CCAACAC	ATTTACGTTGGCCAAGATCTCCCTTATGTTGGCATTCGA/GAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCTAA
WI-15153	40	A G	GCATTGCA			T	CCTTTGCTCTGTAAGTGGGACCAAGGATGTGAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTAGAATCAAAATGGG[G/C]TGACTTTTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGCA
WI-15215	84	G C	TCAAATGGG			CCAACAGGGGA AAAAGTCA	AGGAAAGAGTGGTAAAGCAAAGGCGATCATTTGGATGGAATGATTATGTGTCACGAGCACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA
WI-15225	80	C T	CTC			TTGATTGGCA TAATCACTCC	AATTTGCTAGTGCAAATGGACCAAGAAATGGAAGGGCTATGTAACACAC[G/A/TATGCACACCAG AGCCATGTCAGTGCACAGATCCTCTTGTGCATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15152	51	G A	---			---	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACAGACATGCAACACAGAGATAAACACAAAT
WI-15123	55	C T	TAGGATG			TTGCTTAAGGG CAAACAGAC	

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACCCAGGGCAAAATAC/AJTGCTGGATTAAACCC ATGCTAATGGTTACCTTTATTAGTAATCATGGGTCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGCGCTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGTC/CJCTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT	GTTGTAGTCTT ACATGCTTACG	TCAAGTGGTAATAGCCATTTATTGAGTATCTTGCTTTGATTC/CJGCTACGTAAGCATGTAAGACT ACAACATTACGCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAATAACATTTTGTGCTTTCAGAT
WI-14510	104	A T	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGAAGTACACCCACAGATATTTTGGGGAAGAG TTGTTTGCCTTTTGGGCAAAATATGCATAACAAATATTTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CATTTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTTGCATTTGCAATAAACACCATCATTC/CJCTGAG TCCACAGATAAGTCCCGGAGAGGGGCTTCCCTCCTTCTCGCTGGGTGACGTTCCCTCCACTCCCGAGT
WI-12634	52	T C	GCATCATATG AACTGTCTAGC	GGACAAATTTGT AAACATAGCT	GAAGCCTTTCTGGAATG ATGAGTTTATAAACTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTATTC/JGCTATTAGCTA TGTTTACAATTTGCTCTGAAGGGTCTAGATGTACACCCAGAAAGTGGTATTCTCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC	TTTGCTTGAAGGGCTTGACACAAAGTCTAACTTT/CJTTGTTAAATCTCTGGCTTCTCTGGCTGG TGAGGAGGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCGCAG
WI-12159	28	C T	AAAGTTCTAA AAGACACCGT	AA CCCTCTCTCA	CCACATTTCTGGCTCT CTGTCCGGGGAAGACACCGTGCAAATGC/CJAAAGTGCAGTGGAGAGGGGAGGGTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGCGATTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC	TCCCCAGATTGTATGGAATGCCTAGTGGCATTAGGATGC/CJGTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCAGTACTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAACACACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/G/ TJCCATTTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAATTTCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCT AATCATGGA/CJGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGAAATTA
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCCTCCACCAT GATTGTGA	TCCTG AAGGTTAATGGACTCACAGTTCCATGTGGCTGGAGGGT/CJTCACAATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123	C T	AGTTGGCATT AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC/CJTAACCTCCATGT GGGAGTTTTCATAATAA

WI-14528	62	T G T A A A T	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCAGTGGGTATAATTGA
WI-15347	74	C T A A T T	GACTTCAAAG GAAAGAAACA	TCACGCCCCA AGTCTTIG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/CAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA GG
WI-14546	95	C A G G A C T C A	CCAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	GTATTTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/AJCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G A ---	---	---	TTTATTGGCTGTCTCTGTAATACAATGTGGTGAAAAAC[G/AJCTTTAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGTACTGCAAGACCAAGTGTCAAGGCACATAGGCTGATTATCAGTGG
WI-14580	100	G A G T C T T G C A	CATTCCCATCT GTCCTGCA	CCGACCAAGAT CCCTOC	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTTCAGAACTTCTCAAATAC CTAGTTATTATACACATCCCATCTGCTTGCAG/G/AJGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C G G C T T A	GGCCTGCAITTT GGCTTA	GGCCTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAAACACACAGCTACACACAGGCTTGCATT TGGCTTAT/CJGTGCCCTGAAAAAGAGGGCCGACCTCTTGATAAAGAATGTCT
WI-8039b	97	T C ---	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACCTTGTTCAGTTAAATATGTA/CJGTGTCGTCATGTCATGATTAAATATCCTTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCGACGCCGACACCCACA
WI-8039a	87	T C ---	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACCTTGTTCAGTT/CJAAATATGTAATGTGTCGTCGTCATGATTAAATATCCTTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCGACGCCGACACCCACA
WI-8044	107	C A ---	---	---	CACAACATTCAGAAAGTTTTCTGCATTGTCTCTCTGATGTCTAAAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCATAAGGTTCTCCC/C/AJAGTATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCACAGACATTTGTAGGTTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAGAAATGGAACCTCGGCTGAATGCTTCCCACACT
WI-8550	32	G A A T G C A A C A A G	GGGAACAICA ATGCAACAAG	TTTGGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCAAAAGAGCAACTGATGCCCTCAGTGAA
WI-8057	87	T A ---	---	---	TATTAGATAAAACCCCTTTGTTCCCGATTCCAGGATGTTTAAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTT/AJGATGGACAGCAGCAGGAGGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCCTCACAACCTGCCCTGTGAGGGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG

WI-6192	91	A	G	GAT	GACTGCTAAG GATTTAATTTG	TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCACATGATTGGCAGTTGGCATAATTCTAGTGAAGCAAGTGTTCT GACTGCTAAGGATTAAATTTGGAT/GAATTTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105	T	A	GAAA	CACATGGCAA TGATAATAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTCTCTCACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACTT GTCACCAAAAGAAGTCACATGGCAATGATAATAAAGAAAT/GATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAATTTGGAAAAATAGGAGTAA
WI-6213	164	C	T	---	---	---	CATATGCTGCTTATTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTCAACCACTCTCAAGAAATGTTAGTATGTATTGTCAATTACATGTTT ACTTTTGATAATTGCTCATTAATACTATGTC/TATATAATAATGATAATACAGTAAGTAGGTGATCC TGCATTTGAGGTAAAGCGTAGGTGGAATCCAGATTTCTCTTGAGGAAA
WI-6217	131	C	T	---	---	---	CGGGTTAGAAATACCTTTAAATTTAGGTAAATAAAGCTCAAGGAGTGGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCTTGACAAGCAGCTCAATCAAG[C/T] GGCCCAACCATGGCCCTAGGGTGTCAACAAGTCCAGCAATCATGGCGTTCTCGTATATCTGATCC
WI-6238	175	G	A	---	---	---	AC ATAGTCTTTATTGTCAACGAAGGCTACACGGGATCACTCTCGTTTGTGTTTATGCTTTTTTTTTT TAGAAGGTATCTACATCTGCATTTATTACAGCCTTGTTGGTATTACAGACTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTT[G/A]GTTCCAGACTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTTCATCCAGAACGAGCTTG
WI-6272	86	C	T	TAA	GCATTTATTCA GGGAAACTT	CTGTTTTTGA GAAGACAAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGATTAGTCACTGTACAGTCATATAATGCAATTTA TTCAGGGGAAAACTTTAAT[C/T]TCTCTCCAAAAACAGCTGTGGAAACACCTCAAAATTA GGGATGTTTCATCTAAACACCTTTACTGAAACTTGATTCCTTGGGCCAGAGGAGTGTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTTCGGGCAATAAATGAATCTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAGCTCTGTCTG[C/G]ATGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAAGTCTAGTCTCGCCTCTCGATTTCCTGCCAGCAGTCTCTCTCTCTCTCTCTCTCTGCCCC
WI-6303	96	G	A	CTCTGTCTGC	CCAGAGAAG	CAGCCATGGCT TTGCAG	TC TG ATGCTTTTGCATGATTCTAATTATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTCAAGCCCGCGTGTGATGCTGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGT[C/T]CTGGTT CTCCCTTTACATCTTTTGGGGGA
WI-6315b	193	C	T	---	---	---	ATGCTTTTGCATGATTCTAATTATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTCAAGCCCGCGTGTGATGCTGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGT[C/G]AGTGTCTCTGGTT CTCCCTTTACATCTTTTGGGGGA
WI-6315	187	T	C	---	---	---	ATGCTTTTGCATGATTCTAATTATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTCAAGCCCGCGTGTGATGCTGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGT[C/G]AGTGTCTCTGGTT CTCCCTTTACATCTTTTGGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTATTGCATATGGAAATCAATAG/GJATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAGGGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA/T/A/GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC/A/TATGTGCTTATCAGCTCCCTCCACCCCTATATTTTAAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATAATCCCTGGGCACATGGATCCAAAGAGAGATTTTGACGAGATTTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/G/TJATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTTCACAACAACACGACGCTAAACTCTGAGAGAAAC/C/GJCTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTTACATGGGCCCTATTATTAAAGGACATTTGTGAATGTTCCACTTTGTTTTAA /C/TJTAATCAAAACATGGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTTACATGGGCCCTATTATTAAAGGACATTTG/JGTAAATGTTTCCACTTTGTTTT AAACAATTAACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACCTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTTCAGAGAAATAA AGTTGTCATAT/CJAGCAATGGATGCTGTGTCAGAACATCTGCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C GTCATA	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTTCTTGTCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACAC T/CJACCCAAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTATATTTTGTGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCATTTAATGAAGGAGAGTACTAGGAAAAACTACCAACACAGCATGTGAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC/C/JGGCTAATACAGTGAATATTTTA TGTTAGCAAAATTATAGCTGGTCTGTGATAACCAAGAGCGGTATCTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTAATTAAGGAGATTCJACTAGGAAAAAACTACCAACACAGCATGTGAAC AGTTGGGACGGTGTAAAGGACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAAGCTGGTCTGTGTATAACCAAGAGCGGTATCTGG
WI-6770	53 A G	CAAAACCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTAATGACACAGATCTTCCAAAGTAATCCAAACCCCAACATCACA[A/G]AATATTTCAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6886	151 A G A	GCATTCITCCA AAAACAAAGA	CCTGTGAAGTG ACTATTCCAAT GIT	ATTCTGAGGCAAGGTCAGCAAAATCAGCTAGCTAATCTTGACCAAAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTTACATTTTAAACATGTTAACTCCAAAGCATTCT TCCAAAAACAAAGAAT[A/G]AACATTGGAATAGTCACITACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGATGG[C/A]CTCTTCTCCAGCTTTTGTGAACAAAAAC AATCTCCTAAGGCATCAGAAAGCACTAGTGCAAAATGGTTGTTCAAGTACAAGGTCTC
WI-6844	225 T C ---		---	TAAATACTGCCAACTAGCATACGTCCTCTTGATCATTAAACAAAGGTTATTCCTCCTTG GTATTTCAAATGATGATTATACAATAAACGAAGTTAGAACTTAAATGCACCTGATTAAATATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCTCTTCTCATAAATGGAATTTAAA TATTTCTGTAGTCTTGAGGTT[C]ATCAITATGAGTAGTGCAAGGTG
WI-6824	112 A G ---		---	CGGTTTGTCTACACTTAATGGTTTTTTTAAAGGATTTTTTTCAGGCTTTGTGAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGTACAGAGTGCTGCCAA[A/G]CACCTTTAGAAAAATTACAT GACACGGAGAAAATGCGCTCTTGCTTGAAGAGCTTACAGCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATTC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCCAACATGGAAGTGTCAAGAAACATTCGTATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[C]AAGAATAATTAAGGCCACAAAGTGAACCTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCCAGCTCATATTTATTTGGCACAGAGTGGGCACTCAAATATCTGATGAACITTGATGAACGTAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGGAAGAGAGAGTCCCAACCATATATAAATGTATGAT CAAGTCCCAAGAAACTTGGCTTCCCAAGGAATGTGTTCTAAATTTGGTTTCAAAAGCACACTGGTTCC CACITTTACCACCTT[C]CATGACATTGGACAATAGTACTACTCTTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTAGTAAGTCTCTAGGGACATGACAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTTGGGTGGAGGATACCGCTGCTATTTCCAGATG[C]AAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTTACGAAGATCAAGTAGCCCCAGCT ACAGCCT[C]TGGTGCACTTAACCCCTCTCCTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTTCACGTTTCACAACACACGCCGCTG/GTJGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTGGCCGGAAGGCTCATCTCTGCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTTGGGGCACTCTGTGGGCAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTTGACGATGAGCTTGCAGTGGTCCAAAGCGGGTGTGCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTTCTT TGTTAAATAAATGTTTATAAATGTTTATGAAGCTCATTAACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	GCTGGGA	AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT/GCJACACCACACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCAAAAAACAACCAACTAAC CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/GCJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCAAAAAACAACCAACTAA C
WI-13119a	51	C G	---	---	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT/CJCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGTCGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T	AGCTTTT	TTAGAAATTTT GTGTATTAT GGAAAAG	TGTTAACATTTTATTGGTACGTCTCAGTACAA/CJAAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAAAGAAAGGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAGTGTGTTGTGTGACCATCTTTATCTCCCTGTGGATGAGATGTGACACACAAAGT AAA
WI-12988	36	C A	CTCAGTACAA	GTTT	TGCTATTTCATGACAGACACGTCGAGACAATAATTTCTTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCTTGAGACTTTA/GJATCTGCAAGGGGTTTAAATAAT GCAAAATACACATATTTCCATTTTAAACACCATAATTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTTCCCAATAT
WI-13020a	108	G A	CTTT	CATTATTAAAC CCCTTGCAGA	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGCTCATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCAA/GJTACAAAAAACAAGCATTTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCCAGGATGAGGCAGAAAGCA AGTTGTGTC
WI-12837	87	A G	AAAGTCCA	GCATATACAT ATATCAAGGT ATGCTGTTTTT	AGTTGTGTC

L42611b	50 G C ---			GTCTCAGGCCCTCTCTGGCTGCAGAGCGCTCTCTCAGGTTGCCTGTCGTCGTCCTGCGCCTCTAG TCCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCAGCTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 T C ---			GTCTCAGGCCCTCTCTGGCTGCAGAGCGCTCTCTCTCAGGTTGCCTGTCGTCCTGCGCCTCTAG TCCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCAGCTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAAA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAATGAAAGAA[C/G]AAGAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCCACTTAATCTGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCCATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAAACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATT CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATCTCCTCTTTTCATTAAATTTCTT TCAC[G/A]TTATTCCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTAAAAATCCACCTTAC ACATTGGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATT CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATCTCCTCTTTTCATTAAATTTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTAAAAATCCACCTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGGOC	GAAGGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATATCTTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[C/G]GGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTTCT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTACTCTATTTTGTTC[CT]AGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CCTTGCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTT[C]ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGIATATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGC[CT]GAAACAGAGAGGTTTCAATTGACTCTAACTGAGTAC[T]A[CAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGC[CT]GAAACAGAGAGGTTTCAATTGACTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCTTCTCTCACCCAGTCCACATGGTGCCAAACATCCACATTCCCT ACATCCTCCCACTGGGCTGCCCTTTCACAACTCACC[A]A/GIACCTGGCTTACCGGGAAGCATAA GCCAAAGCATTTAGTCTTTTATGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATCTAATC CCACATGACAG C	ACTCACTGCTGCTGTTGATTTAATCAACCTAGCC[G]A/GCTGTCATGTGGGATTAGAATAAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACACGTAAAGAT ATAACTTCAA
WI-991	37 A T	---	---	TGCATTCTATTATGCACCAATAATAACTTCTGTACATAT[C]ATTATTGTATTTCATTATCACAAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACAAACACTGACTCCTTTTCTCCTTTGAAAAACAAGGC
WI-1011	70 G C C A	CAGTATCTGA AGTTTTGTCT CT	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATCTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTGTCTCC A/GC/JAGAAAGTCAATTTGTAGGTGTTCTCTGGCGTTTGTCTAGCTTTCCATTTTCTTAATACACTGC CGTCTTAAGGGAGGCTTCAGAGCATTTATCAGATGGCTGTTTGTGCTGCAATCTGTGCACTGAAG
WI-5381	178 A T	---	---	TTCATGCAGAAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGCTCATGAAATTTGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAACTGGCAATTAGTTTGTATTTACTAAAAACACAAATGT TTAACTTGGGGTCCACAAACAAAGGATATGTTGGCAATGGTATTTCTGIGATG
WI-5791b	76 G A	---	---	CTATGTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG[G]ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCCAAAAGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGCCACCCTGTTTGT TAGGAA

WI-5791a	44	C G	---			CTATGTATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/G/ACAAAGATGAGAACAAGGTC CTAGAACTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAGAACTTACATCAGATTGTGCATTTCTTATTTTGCCACCCCTGTTGT TAGGAA
WI-5406c	120	C T	---			CACCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5406b	118	C A A		CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5406a	42	A G	---		---	CACCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAG[A/G]GCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5798	48	G C T G		TTATTCCTCC TTGTTTCCTT	ACTGTTAGAAA ACCAGTATTTT TCAAT	CCATTCCTCTCTCCCTCTCCCTTATTCCTCCCTGTTCTTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATCTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A T T		TCATCATTTCAG T T T	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTTGCTTCATGAATTCATCTTTCAGTTT[A/J]TAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G		TCCAGAGAA AAATCCAAAG G T T A A G	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTTGTGTTTA GAAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G C T G C A G T C G		TGTCATTTATG CTGCAAGTCG	TTACTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTG[A/J]AATTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCG[A/G]A ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCAACAATTA
WI-5481a	29	G A A A T T T		CCAATTTAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTG[A/J]AATTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCAACAATTA
WI-5492	38	T C	---		---	TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCA[T/C]CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATAATTTGCAGACCAA

WI-5826	134	T C	---	---	---	TATTTTTTTTTCTCAATTCCTGGAGACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAATTACTCTTTACAC
WI-5546	40	C T A	CCCAATACITTT TTCAGGTGAA	CCTGTATTTTA GCAAAACATGGG	---	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C]TACCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAAGGGAATTACAAATGCTTGAGTGTAATTCGTATGTTGGGAAATAT TAGAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG CCCAGG	---	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGTATTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTAGAGT[C]TCTGGGCAATTTGTGCACTAGTGTGAGA TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATAACTCTGATGATACCTGTTGATCCCTGAA TCCTGCAATATACACATGATCAATGAT[C]TJCCAATTTGAAAAATTAAGCTTTTGAATGTTTTCCTCA ATG
WI-5836b	161	C T	---	---	---	TCGGGTATTAGGATGCGTTACCCCTCGATGATGCGGTTCATAAGGAGGTGGGA[C]TJGACAC ATTACTCTCCAACCTTTCATCAGAACACTTCAACAGCG
WI-5573	58	C T	GTTCAAGG AGGTGGGA	AGAGTAATGTG TC	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTTCCACCCCTCACTCTTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGACGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTC[G/A] TTTTGCCATTTCTGTATATCAACAGAGAGAGGAGGGTGG
WI-5850b	134	G A	---	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTTCCACCCCTCACTCTTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C]TJGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGGAGGGTGG
WI-5850a	92	C T	---	---	---	TGCTGATTGACACATAGTTATCTGACAGTAATCATCTAACATCAACATAATCTTTCTGCCTG TCACACTAATTTGCAAGCATTCATTAATTGACTATTAAATGAGCATCGTGTCAAT[C/A]TJGAGTGT TTAGGTTTCTCAAGAGAAATTAATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612b	125	A T	CTATTAATGA GCATCGTGTCA TTC	TTCCTTGAGA AACCTAAAAC ACTG	---	TGCTGATTGACACATAGTTATCTGACAGTAATCATCTAACATCAACATAATCTTTCTGCCTG CTGTACACTAATTTGCAAGCATTCATTAATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTAATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	---	TGAGAGCCAAATTTATCCGCAATAAA[C]TJTTCCCAAGTCCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC
WI-5636	26	A C	GCCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	---	

WI-5865c	103 C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTCAATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAATTTAAAC[G]AAATATTAAATTTTATTTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAATAATAATTCACAG
WI-5865b	99 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTCAATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAATTTAAACAAATATTAAATTTTATTTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAATAATAATTCACAG
WI-5865	165 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTCAATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAATTTAAACAAATATTAAATTTTATTTTACAGAGGAACTC AGAAAGCCAGAAAAATGACCAAGACACAGTTAAACAGTCTCCATCTTCAAAAGGTCACAGTCTTCC AGAGAAGACAGACAATAATAATTCACAG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTCAATTAGTTGTTAAATTTTGTGTTTTCATAGCATGGATAATATTACAGAA AAAAAATTTTGTACATATCAAAATGACTGAAACCTTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTGAGCCTCTCAGTTTTCATCAGTAAATTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCTGTTTCAACTCTCATTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTTC AGAAAAATAAGTAAATG
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG AGAGTAAAT	GACAGAAAAAG AGAGTAAAT	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAATA[G]GJC CATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAAACGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA CATTGTTGAAAAACGAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61 C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAAACGAAGCCGAGTTTTCGATTACACAGTT GCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G]ATCCCCACGAA ACATTGTTGAAAAACGAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187 G A ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAAACGAAGCCGAGTTTTCGATTACACAGTT GCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G]ATCCCCACGAA ACATTGTTGAAAAACGAAGCCAGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5944	52 A G GGAATCTTG	TTCTCACCATG AACCTTGA	GGGTGGGATCT AATCTG	AATATCTGGCCTTTTCTCTTAGGAGGAGATTTCTCACCATTGGGAATCTTG[A]GTGCAAGTTAGAT CCCCCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTCTCAGTCTTCTGCTG
WI-5967b	148 C T ---	---	---	GAGTTTAATGAATCCTGTTCCCTCTCTAAAAACCTCCTGTTCCCCAACCTCAGATTCAGCAGATATT CTTTCATGGGTTATTTGCCCCAAGTCATGAGGAGATGCATGTAATTGATCATTTTCAAGAGTGTGAG TAATGCTTGGTA[C]TTTGTCTGTGCCGTATCTGCTCCATCACCCATTCACCTATTATTCCTATTAT GCTGAATGAAACGGTTATATTACAG

WI-5967	165 C T ---				GAGTTAATGAATCCTGTTCCCTCCTCTAAACCTCCTGTTCCCCCACTTCACATTACAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGCGTAT[C/T]GCTCCAATCACCCATCCACTTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---				GGGTAGATCCAGAGCCACAGGTGAACCTGCGCGGTTATGAAGTCTTTGGGCCA[G/C]GTCGTGAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCACACTGTGCACCTGAGCCCATTTGTAGGGA GCATTGAACCAAAACCCAGCGACACTGCTGACATTTGACITTCAGCAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATT AGCATCTACA	TGAAAACCCCA GAACAGTG		GACTCTGTCTCAAGAAAAAAATTTGAAATTTGAATAATTATTAGCACCTCTTAATTAAAGCAT CTACAAGGTACTTAT[C/T]GACTGTCTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAAATTTGTCTTTT CTC
WI-6450	45 T G TGCACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTTGTTACTT CT		ATAGGACAGTTTTTCTCCAAATGACTTATTCTATATCTTGTCAAT/GIAGAAGTACCACACATTTCA AACAAAGCCAGGCTATGCCAGGGTGGGATTTTTCACGGTCATGTAATATGCATGTAAGACTA TTTTACTGGCTTCTTTTATGCATAAAACAAGGATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAATATAGTCTTTATAGAATATGTGTTTAGAATAAAGCCACA AATTATTCTATAAACCAAC[C/T]AAGGAACGAGGCTCAAAAGTGAACAAAAACGGCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAATATAATCCGTGACCTCTTA
WI-6461	88 C T ---				GAAACTATCCTTTAGTGGTGCCACATTTTCTATTTCTGATTTCTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/T]CATTGAGTGAACACTAGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT CCTGG[G/A]AATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466c	141 G A TTTGTCCTGG	TTTTCACAGTC	AGTCGCATGOC AATTTATAATT		GAACTATCCTTTAGTGGTGCCACATTTTCTATTTCTGATTTCTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/T]CATTGAGTGAACACTAGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA	ACTGAA		TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTGTCTCCATTTGCCACGTCCTCCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCT[C/T]CTCCTCAGAAAGACACTTTGGCCCT CATAGGCATTCCATAGATAATTGTTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104 C A ---				CCTCTAACAAAGAAACCTTGACTTCTCTCAACTCAAAAAACCTTCTCTAATAATTTT[AG]AGTAACCA AAATATTCCTTCAATAAATAATCTCTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCAAC
WI-9720b	55 A G ---				

WI-9720a	47 A G ---	---	CCCTAACAGAAACTTGACCTTCCCTCAACTCAAAATACCCCTTCTCT[AG]ATAATTTAAGTAACCA AAATATCCCTTCAAAATAAATAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CAACC
WI-9825	123 A T ---	---	CACGCTTAAGGCAGGATGGCTTATGAGATACCTTTCGCAATGCTGTGTCACACCTTGAATCTGCC TGCTGGCTCCCTTACCTTCTCTGTCATGTGAGATGAAGGCTCAGGGTCTG[AT]GAGGATTAG TAAGATCTCTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTACCAGGGTTAGTTTGCATT TAAGAATTGCCAGCTTTTGTCTGTCATCATCTTGAACATTATCCACATG
WI-9748	74 C G ---	---	CCACTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTTCTAAATTTTATATGTTTACCCCTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTCTCTGGAATCTTTTCAGAA TACAGTTATGATGTCCTTTTATATCCCA
WI-9943	91 T C ---	---	TGAGGCTATGATTCAGATTTGTAGTGAATACTTATTAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTC[C/AT]TTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTTAAATATGCAATTCACACCTTCTCTTTTGTCAATTAGGA
WI-9891	39 T C ---	---	AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCGCTCTT[C/AG]TGAGCCTGTGAACCCCAAGAC GGCTGGTCATCAGTGTCACTCTCTCTTTCGGACAACATCTTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAAAATAATCTGTTTAAATAATCTTATTAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCATCTACACAAAAAGGATTGCAAA
WI-9897b	84 C T ---	---	CTCAGAATTATCAGATCTTCCCAATGTGATGTTCTGTCACACATCTATTTTTCCTCAAAC ATTTATCTAGCCTGTAT[C/AG]TCAAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	CTCAGAATTATCAGATCTTCCCAATGTGATGTTCTGTTCTCAACATCTATTTTTCCTCAAAC ATTTATCTAGCCTGTAT[C/AG]TCAAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGTCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTTCAGACA[C/A]AGCCCAAGAAAAAGCC TGATATTAAAGAGGCACITGCATTAA
WI-9935a	42 C T ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGTCACACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTTCAGACAAGCAAGAAAAAGCC TGATATTAAAGAGGCACITGCATTAA
WI-9983	146 C T ---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCTCCCATTTCTTGTCTTGA TCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAATCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA[C/T]AGACACAAAGACAAAGAGGTTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A	T	ATCT	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTTGGTTTATTTATGTGTGCTATATAATCAATGTTCTTA ACATTCAAATAAGATCTTTTGGTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAT CTA/ATTTCCCTTAAGCACAGTAATCAAGGCTTCTACCCCA
WI-10020b	122	T	A	TTT	GCGAGAAAAG AAATCATGAC	GACTGTTAAT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCTATCTTGAATCGTATTAATAATTAATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTATTTGGCGAGAAAAGAAATCATGACTTTT/AAJAAAATACC AGACTAATGATTAAATAAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCAGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T	C	ATAAAT	TGTCATCTTGA CTCGTATTAA	AAATTCITTTT AGAGCCAGTTA AC	TTTACTTCATTGTCTATCTTGAATCGTATTAATAAATAA/AT/CTGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTATTTGGCGAGAAAAGAAATCATGACTTTT/AAJAAAATACC AGACTAATGATTAAATAAATAAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCAGCTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	TTTACATG	CCTTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCTTATAATAAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATAATTTGGTGACACTCTGTTTATATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATGCT/AAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C	A	CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAAATTATAT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCT/AAJTTATAATA AATAAATTTGCAGAGCATCTCTCTCTATGCACCAGATAATTTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T	C	CAAACCTCT	TCTCCTGTCC CAAACCTCT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCTCCCAAACTCTA/AT/CT/TTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAGACACCCCTTATATTAGT
WI-1319	40	A	T	ATTCCTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTT/AAJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAACTTAACACTGGTCAGATGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T	C	CTCTT	CTGTTGATTTT CTACCTCTATT	GCITTTGGAATG TATCCAAAAGT TT	AGCAACGTTGACAACTTAGTGAGGTGTAATCAGAAAGCATCTATATTATTCACCAAGTCAACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATCTCTA/AT/CT/AACTTTTGGATACATTTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGGCCAGCC
WI-2572	61	C	T	AGTGAGTTGTGCACAAATTTGGAGACATTTCTGTGACCCCAACTTAAACACTTCTCCACAC/CTAC AAAGTTAAACACTTCAGTTACCAAGGTGATGATGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGGCTTGT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAACGCTGAAGCAACCAAGGCTTGTTC/TCTACCCCTCTTAGAGATAAATAATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGTTTGTCTACCCCACTGGAAGCAGAAATATCC TTCAAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTCAGGG T
WI-10391	32 A G	CTGCTCAGGT ATGACTCCCA	GGAGTTAGGA GTCAAGAAGTT GA	CCTCCGTTCTCTGCTCAGGTATGACTCCCA/GTCAACTTCTTGACTCCTCACTCCCATCTCGGTG TCTGCTCCCAAGGGAGCATCTGACACAGCCCTTTGCTTGTGTGACAAACAGAACATTCAGAAAG TGATGCTGGGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCCTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTCCCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAGCTTT CTAATAGCAA/W/CJAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGGTGCTCAAT AAATATTATT	AAAATCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTT/CJTCAT ATTTTCCAAATTTAATACTAGAAATTTTCCCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACCTCAA ATTGCTTTAAG	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATTTTCTATCTCACCTAAATTTATGCGTGATTAATAATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTAA/C/GJGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
WI-11153a	33 C A	GGGAATATTC TATCTCACCTA	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTTCTATCTCACCTAAATTTATG/C/AJGTGATTAATAATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
WI-2616	125 T C	CACAATGTA ACAAGAAATTG	CCATGGCTGTA GTCCAGT	GTTGTAAACTCCAGTATCATTTCCCTCAAAACCAGCTTAAATCACAAATCACTTTTCTTCTGTA GAGCTCAAACTCAGCTGAATGAATTTGCTGCACAAATGTACAAGAAATGATCCTAT/CJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTCAACAAAGTGAATTTATGACCAAAATGAGA/C/TAAAT TTGTTAAAAAAAACCTCAATGAAGAGACAAATATAGTTCAAAAGTTCAAGTTCAATATTTGT ACCTACAAATAGGGATAGTCATGTTGGCAGACTTTCTTTCTTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCCATATTTTAAAGGAGAAATTCACCTTTTCT CTGTTGGATGATCAGGTTCTGCTCTTCCCAATCCAGAGGAGGACTATTCACCCCATGGGGTCAT AGAGAGGATTAAACAGGGGTGATGCCCTGCAATGGGAATATTTGAAAACC
WI-10656	59 T G	---	---	---

WI-11169b	154	T G T T T T	T T A C C A A G A G T T T T C A T T C A	C T A A C T T A A A A A T C C T C A T T C A A A A T A T A A	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T C T C T A T C G A G A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A T T A A G C C T A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A G A G A C A G A C A T T G J T T A T C A T G T T C T G A T A A T T T T T T A T A T T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-11169a	95	A G T T G A A A A	A A T A A G T G A A A G T A A C T G A C	A A A C T C T T G G T T A A A A A G C A C T A C T T	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T T C T C T A T C G A G A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A T T A A G C C T T A G A G T A G T C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A G A G A C A G A C A T T T A T C A T G T T C T G A T A A T T T T T T A T A T T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-10685	25	A G ---	T G C C C C T G T C	--- C A A T C T C T A A A T T C A T G T G T A G A C A C A	C A A G T G C T T G G A C C T T G G A T A G T C A G A C C G G C T G A A G G T T G G A C A G T T G T T G G T T A G G T T G G A G A C C A A A A T T C A G T C A T C T G T A A T A T A G A T C T T G T C C T T T T G G G T T A C C A C T A G G G G T C A C T A A A G A G A G A T G G G A G A C A G T C A A T C T T G T C T A A A T A A T C C A A A A T A G C C A T G G G T T G G A C A A A A T A C A A G G T T A G T G T C T C T A C T T A A T A G G G C A T A
WI-10686	133	C T A A G G	T G C C C C T G T C	T T C A T G T G T A G A C A C A	A A T A A C C T G T G C A C A T A A G G C A A A T A C T G A G C C C A T A C A G A G T G T T T A T G T T A A T A T T A T G A A A A A A G T C A A G A G A A C A A G A T A T A G T T C T G C T A G A A T A C T T G A A A T C T G A T G C C C C T G T C C A A G G I C T T G T G T C T A C A C A T G A A T T T A G A G A T T G A A T G A A A T G G C A A A A T T C A G A A A A G G G
WI-11175	77	T A A	A A A T G A T T C T T T C T G C T C A A G	C T G T T C T C A C A T T C T T T T T G A A A A	G G T A G G A T G A T T C T A G A A T G C C A C T T A C A G C C A C T G A A A T A T A T T G C C T C C C A A A T G A T T C T T C T G C T C A A A G A G T A J T T T T T A A G T T A C T A C T A T T A T A T T C T G C T T T T T C A A A A A G A A T G T G A G A A C A G T A C A A A A T G T T C A G T A T A G C A A A T T A A A A T T A A T T A A A A A G T A G A A A A A A A G A A G C C A A T T T G G G C
WI-10694	144	A G T A T G A G T T T C	T G C A A A T G C T T T A T G A G T T T C	G G C A T T T T G T A A A G G A G G A A A	T A G A G A G T C T T C A G T T C A G G T T G G A G G G T G G T G A G G T G A G A T T C A C T T C T T A G A A G C A C T G G C T A T G T A C A G A A A G A T A A A C T C T G A G A A G A A C T C A G T T C T A A A G T T C A G T C T T G C A A A T G C T T T A T G A G T T T T C A G J T T C C T C C T T A C A A A A T G C C A T C A A T T C C T C A G G A A A A A A A A A A A A G C T T T C T T
WI-2716	23	T C C	T G A A T T C A T C C A G A A A A A C A G	T C T C T T T T C T C T C T T G T T G T C A T T C	G T G A A T T C A T C C A G A A A A C A G C T C J G A A T G A C A A C A A G A G A G A G A A A A A A G A A T A A A G G T T T T T G T A T A C G A C A A G T G G C T C A A G C A A T T T C T C T G T C C C A G T G C A T G G A G C A G T G
WI-10719	115	T C G C C A T T C T A G	T G A C T C T C A A G G C C A T T C T A G	G C A C T G C C A G C A G C C	C A G G C C C A A C T C T G C A T A A G T G T T T A G A C A G A C A C C T C A G T C A C A C A A A G T T C T C T T G T A T G T G C C C A C C A T A A C A G T T A C T G G A G G A T G A C T C T C A A G G C C A T T C T A G T C J G G C T G C T G G C A G T G C T T T T C C A G C C T G C T G C C C A T A A C T A A
WI-10721	40	A G C T T G C C A	T G G C T C T G C T A	G A A A C T C C C A C A T A A A T A A A T C T C A	C A A C C A A T T C A G A T T A A T T T T G G C T C T G C T A C T T G C C A J A G A T A G A T T A T T A T A T G T G G G A G T T T C T G A A G A T T C C C A T G G T A A A T A G T A T C C T C T C C C T G C T T A G G T T T T G A A G A A G T T G A A

WI-11204b	88 T C ---				GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAAACTTTCACCTTTT[C]AATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTTCAGAAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA	GTATCACTTAA AATGTACATAAA TACCTTT		GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAAACTTT[A]CACCTTTTATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTTCAGAAAG GCAACATC
WI-10732	80 C A ATTGGTTCACT	GCTGTGCTTC CTGTATGTACA	AAGAACAATG CATAACAGAA CTTTAA		ACATGTATTTCCCTTAGTGGTCAGCCCTTCCCTACCCCAAGAAATATCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACT[C]AJTAAAGTTCTGTTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACCTCTGTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTT CTGTATGTACA			TAGTCTTTTCTTTGTACGAGTGCATAAAGAAATTACCACCTCTGCACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACCTC[A]TCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATTCAGTGGTGATTTGAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---			---	GAAAAAAAGTTTAAATGGATTGCTTAGTTGCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C]T[A]TTTTTTCTATAATTTTCTTGTAAGTGATGGATTTCTATAAATTAGGAACAGATATTT ACACAGAGAGAGACAGGATTGCTTGAATTAGTATAACATTCITTTATCCAAAGCCCCATTCACCCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAAATAT TCCAAAAAGT	GGTCTCTAAT TTTCTACACT TTCT		ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---			---	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GCGTGG	CATACCACTGC AGCGTGG	CCTGGTAGCCA AGTTGTGA		AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAATGCTAAAAATGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCAGTGGCTG G[G/A]TCACAACTTGGCTACCAGGAGAACCTGCACACAGACTTCGTAATTGCTTTCACAGGGCTACTGG AAAGCC

WI-11222a	25	C T A	GCCACAGTGG AATCATTAC	TTTAGCATTT GCTGATTCG	AGCCACAGTGAATCATTTACACTA/C/TTCGAAATCAGCAAAATGCTAAAAATGGGCTTTGGATTT TGTTTTGTTTTTCCATAGACCCACCGTTGAACATATTGTTAAACATTTACCAGATACCACCTGCGG CTGGGTCAAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATGCTTTACAGAGCTACTGGA AAGCC
WI-10775	39	C T	TTTATGCCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTTATGCCATATTAAATCATTACACTC/C/TACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCAGCTCAGTAAGGATATTCCTGGCAGATAATCATTTGTTATCATTAGACATTGCA GGAACCAACCATATGGATGATAAATGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165	A C ---		---	TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAAACAAATGAATTAGAAAAATGTCAGTGGTTC TAGTACAGGAATCAAAATTTGGACTATGAACA/A/C/GACATAGTTGCTAAGGATATTCACACAAATTAT TTCATGA
WI-10778	62	A G	GCAAGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/G/G TCCATCTCTGATGTCAACAGCGAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21	C T	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC/C/TTCACAGGGTCCCTCAAAGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGACATCAGGGCCCTAGTCTCTCTGGGACAGTGAAGGGCCACCAACC
WI-10810	58	C T	CATCTTCATGG GCAGGAATT	CAAACCCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGGAAAGCATCTTCATGGGACGGAATTC/C/TCATTT CTGTTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10828	23	T C ---		---	GGACCAACACAGAAATTACTTGGCAT/C/JAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91	G C	CATTAACTGCG AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAACGAGGCCATCCACGCTGCTCTTAGCACAAAAAATAAGATAACATCATTTCTGAATG GGCACATTAATCTGCAGGCTCTCC/G/C/TTTCTAAGTCACTGACAGTGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGCGAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10834	96	C T	AGAATTTAACT GTTCAAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATGGCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAAACTATA AAGAAATTAACGTGTTCAAAAGTGTGTTAAT/C/TTTAAATACCAATTTTATAGGCCACCAATTAACCT CTGAAGAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T C ---		---	GGATGATGTTCTGTGGTCCCTTA/C/JAAAGCCTCTTGCATCCCAATGTTGTAATATTTATTTATCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCT

WI-2296	81 A	TGTTACTTTGA TCTTTTGCTCT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCTAGAAAGGCTCAGGCTTTAGAATAAGTTGTTACTTTGA TCTTTTGCTCTGACAGCCAGTTAGCTGTGATTGAGAAAGTTACATTTGTTGTTG
WI-2300	77 G	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTATTGAGCGGGCAGGTGGTAGGCACAGAACG CAGTCATACGTTTCTTTAAATGACCCCAACCATTAAGAATAGCAATTC
WI-2371	55 G	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAAGGCTGGTCTTGTCTTCCAGCTCTGTTGGGGGCT GTCAATCTTTGACATTCCTTGTCTTGACGCTGTATAATCCAAATCCTTGCTCCAGCTTTACATGATGT TCTCTCGTGTCTGTG
WI-2395	122 A	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAAATCCTGAATTC AGAAATAAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTTATTAGTAACAATCTTTA CAATTACACAAACCCA
WI-2437c	192 G	---	---	CACAGCCACCACCCCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGAG/GA/GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	---	---	CACAGCCACCACCCCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	---	---	CACAGCCACCACCCCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGAG/CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG/GA/GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTATACAAAAACACAATGTAATGCT ACATAAAATAATTGTCATACATATTTGTTTAGGAAATAATGACAGAAAAAAGCC/T/CJGTACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C	CAGAGTCTGG GGGAGAAGA	TGCCATGCTT TATCTGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG/C/AJACGAGATAAAGCATG GCAAGACCCACGCTGAAAGTATCCAGGGTGTCTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAGAGAAACAGAGGAGCGTT

WI-2906b	77	T A ---			---	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATCTTCTGGAACCTTTGCTGGAATGCTCTTCCCTCT/AJGAGCTTTGCTGGCTTACTTTTCTTTTCCCTTAGGTTTTCAGCTTCAAAGTGACCTCCTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50	A C TCTTGCTGG	GACACCTTCAT		AGAGCATTCOA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTTGGACACCTTCATCTTCTGCTGG/AJCTTTTGCCTGGAAATGCTCTTCCCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175	CT ---			---	TACTCCTCATCTCATGTCCCTAGACGTACTCAGATTCATGCCCCCTGAACATTTATTTCCCTAAATAGATTTCCACCCCCCAGCACTATTTACACAGAAACAGCATGGAGGAGTTTGGAGCTGGCTCTTAGAGAACTTAAAGGACAGTGGTTTTCCATCTGTCTTCCA/CJTAGAGATCTAGGGTGTCTTTGGAAACCCTTGG
WI-1851	136	G A GTGTTAAGTA	GCATTGAATT AACTATAGAT		TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGGAGGACACAAACATTTAGACCATAGCATTGAATTGAATTAACATAGATGTGTTAAGTAATTAATTAACATGGTACA/AJACAACCTTCAGTTTAAACATTGCTAGTGATTCATGTGGATACCATGTAACCTTCTTACATCATGTGA
WI-3000	62	G A AGAGACCCC	CCCCAAACAC		CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTGAGCACCCCAAAACACAGAGACCCC[G/A]TGAAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177	G A TAGTC	TTTTCTCCCTT CTTAAAGAGA		AAAGTCGAATT GCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCCGCCACCCCGGATATTTTACTTAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTCTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAAATTCGACTTTCTGTAGCCAAGATT
WI-3167	37	T A TAGATTC	AAATTCACCC ACAGATCTAT		TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTCACCCACAGATCTATTAGATTC/T/AJACCCCATCTCAAAAACATATCACATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A AGATAAAGA	GTGGAGTGGGC		TCACTCAAACCT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGCAGGTAGGGAAGGTGGGCAACTTGCAGCAGAGAGAGGGAAGAAAGTTTCAGACCCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAGATAAAGA/G/AJCCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAAG
WI-1775	47	CT TTTTCTCTG	CCTGCATGGTC		AGTTGAGATTT ATGACAATGAT	ACTCCACCAACAGTTTGTGAGCCCAACCCCTGCATGGTCTTTTCTCTG/C/TJTTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G A ACAT	AGCATATTCA TTGATTTCCCT		GAGGACTTAAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCCTTACAT/G/AJCAAATGCTCTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCCTTAGGACITTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCCTTAGGA

WI-3416	33 C T GTC	CCAAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTTAAG AG	TCTGGTTCTCCAAGTTGTAGCATTGAGAAGTC C TCTTTAGAGGTAGTTGTGCTCGCTTAAAG TATGTTTCAAGATAGTATCTCCCTGTTGTCACCTTCTCCAAACAAGTGTACCAACAGCAATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACACACATAATTAATCCCATTTGCCTAAAAGACCAGG TCCTATTCTACAACAACAGAAAATTTAACAAAATTTGAAAATCAGCTACTCTCTTTAGGCCCATCAGAG AAT C TGAAGTCATGGGGAAAATTTGATGCCATGTGAATTTGGAGAAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTTATGAGGTGGT G ATJGGGAGAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACG
WI-3453	70 C T ATCAGAGAA	TTCTAGGCC TATCAGAGAA	TCAATTTTCCC CATGACTTC	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC A G GTATTTTATGAGGTGGTGGGAGAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACG
WI-3474b	109 G A ---	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTCTCCCA	TTTGACCCCATACATGAGAAATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCT C T T GAGGACAGGGTCACCCAC
WI-3474a	90 A G AC	CCTGGGTTTCT GGATGTCT	GGGTGAOCCTG TCCTCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT G C ATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3502	79 C T	GGTTTCTAAC TGGATATAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT G GAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3500b	146 G C CATCT	CCATGCOOCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACTTCTACTACTGCTGTTATGATGCACCT G T CCTTTTGG ATAGATGGTTGATAGGAGATGGTTTAAAGACACAATTTACCTTGTGTTTCCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCACAAAGCCTTATGCTTAC AAAGCGATGTTGAGATACCACATTCATGAAAAGTAAAAACACACACACAAAATATGACATAAAA T A C JAAAAACTACTATAGTTTATGAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCATTCCAGAATACTCTCTGTCTTCACTTCACTTTGACTGCACAG
WI-3600a	78 T G ATAGTTCTG	CCATGCOOCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCTAAAATGTGAAACCAAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAAC T C JACACCGGTTCAATGAAAAACAATGATTTGGTGAGCCATGTCCCTTATTTAATGA GATCTGGGCAATTAATCT
WI-3678	125 G T ---	---	---	---
WI-3687	67 A C ---	CCTCAGTTATG TATCAAAATGA	GGTCAACCAAT CATGTTTTT	---
WI-3735	72 T C AAAAC	---	---	---

WI-1819	51	C T	---			GAAAAAGCAGGAAGCCAGGACGACAAACATTTTGAAAAAGTCTTTTCAGCAC[C/TTTTCGTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTTAACTTGCACAGAAATGCG CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAAATGTGGAAGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	---			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTTCATCATCTCTGTCTCTG[C/GA]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCAGCAAT[C/CGGATGTACCTAGT ATGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTCCGGTGC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[C/CGGAGAGGACACCGACGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGCGAGCCACAAAGGTGAGGAAGCAAGGGTGTGCGCCACT
WI-3901	114	A G	---			GGACCATTTGCTCAGAAAGTACATTCAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCCGCTTCCCTCAGTACAAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C T	CC	TGATCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAACCTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTTCTTCAAGACTCACAG[C/TAACCTCTTCTTCTTCTAGACCTATAACTAG ACTCAAGTCCAGCAGGCCCTTAAAGGTAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTTCCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAAGGAGACGAAGGTC
WI-4091	84	A T	GTGATGCTTA GTGATGCTATG	TTGAGGTCTTA GTGATGCTATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTGTGCAATTTATTGCTCTCTTATGTAAACAAATCACCAACATTGAGG TCTTAGTCATTGCTATG[A/T]TGATAACAATAATTGTCACCTTAATAGGAACCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTCTGTAAATAGGAAGTCTGATTAGATGCCCTTTTGGGTTAGGTTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTGTGTTTCTTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGTCATCCCTTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAAATCTGTTTGGCAATCTATTAAAGG CAATATATACCAGCAGTGGTGTCTAGCAATTTCACTGCTGGGCATTACCTTAACATAAATGAT

WI-4177	68	T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATACATTTCCAAATGACTAGTATGAATAAGCACGTTAAATTTACCTATTATATTT AT/C/CATCATGATTTGCTGCTCTTTCCAAATTTACTACAAATTTGATTGTCACATGAGGCACATG ATCCCATTAACCCCAATAG
WI-4199	51	A C	CTCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCAAGTTAGTCAATATAAAAAA/A/C/CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24	C T	CTGCACTGGT CTGCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGCTACTGGTCCCTGT/C/TTGGTCTGTTCCCTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCACTAAGGTATCAGGTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-4250b	117	A G	---	---	TAAGTGCATTAACTGTACAAGTCCACAATACCTCTTCCACCAAGTGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94	G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCTTCCAC G	TAAGTGCATTAACTGTACAAGTCCACAATACCTCTTCCACCAAGTGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGG[G/TTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68	G C	TGCTCCCCCAT CACCT	AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGGAAAGTCCCATCCCTCTGATACCTTGGTTCCTCCCATCACCT [G/C]CCTTACACAACATTGAAGTAGGCCCCATCCAAACACTGGTCAGAAAGATGTAATACTGTCGAC
WI-4256	57	C T	---	---	ACAGCCTCTTCAATGGCAACATCAAAAGCACCAAGTAAAGCAGAGGCAAAATCTGG[C/TT]CAC CATTGGAAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAAATGTTGGCCTT
WI-4325b	71	C T	---	---	AGTTCACTGCTAGATGAGTAGACCATGTTGTTGTTTAAATGTACATGGGCAGGACCGGAAATGG GATG[C/TT]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C T	---	---	AGTTCACTGCTAGATGAGTAGACCATGTTGTTTAAATGTACATGGGCAGGAC[C/TT]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4347	158	A G	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCCTGTACCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCTGTATCTGTTCAAGGCC[A/G]GAATCGTCACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117	T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTTCTGGGGCAAGTCTGGTGTGTGCTAGGTCAGAGGACGGC ACCTGAGGGACACACAAACAGTGGGACACAGGGGTACTTGTATCACCT[C/CT]CCCGCAACCCCA AGCAGCACAGCTTGAGTCCAGGAAAGACTCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA

WI-5204	54 C T	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTGAGGGGAGCAAAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA CTCAAAA	AGATAATTTTG TAAAGATAGTT TTCCG	TTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A T A A	TTGTATCAAA GAGATGGGT ATATAA	AATTAAGAA ATCTTTACATG GTCTTT	CCCTGAAATGTGCTTTGCTTCTCTCCAACTCTCTAGGGAACCTTTTCATGTGAGGTGAAGGTTTTGA AGAGTACTTTAATTAACCTGTATCAAGAGATGGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCTGTTAT GCATGAACCTTG	ACACATTTCAATTTTGCTTTAAGTTGAATTAATTCAGAAAAATTAAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCCAGGTTGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C C	TCACTGTTATT TTAAAATTAT CCTTCC	TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATTAATCTCC[A/G]TGAAATTTGGTGAAA GGTCAAGAAATGAATTCACACTTTTAGATTTCTGAAATTTTATTCGGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACAAACAGAAAGTATATAAGAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAAACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTTATTTCTCTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA TAATC	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T C T G A G T	CAGTGGTGAG GATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCATTTCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAAGTAAGTCTATCTTCTGAAGATG[T/C] GAGTCTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110	A	G	GCACCATGTGG CATCC	GACAAATGCAGC CATGCA	AGCTTTTCCCTTTCTTAAATAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCCAGTGCATGGCTGCATTTGTCCAGTGC AAATGAGACAACCTTCCCTAT AGCAAGCATCTGGCAAGCCTGGTGACCAAGAACATTAATTCACCAACACCAACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAACTCCAGTCCAGTGCATTAAGGCCAGTTAACTTATCTCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAATGACTCGGTTGGCTGTACAAAGCAT AAACAGAACGCTTGCAAAATATGGTT/C/CCTCCTTGCTAGAAACCATTTGAT CAAAGGTAGTTTAACCTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTTTAAAG/G/CJAGAGAGATGACCCATCCATCTCTGG GCTTCTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-4582	225	T	C	---	---	TGTTTAAAAACCATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAACACGCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/C/JCTTTGCTTTTTTCCCTTCTCTCTTTCTG CCCTCTTTTAACTAT TGTTTAAAAACCATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAACACGCTAC TACCAATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTGCTTTTTTCCCTTCTCTCTTTCTG CCCTCTTTTAACTAT CATTTGGGTGCT
WI-1965	105	G	C	AG	GAATGGATGGG TCATCTCTCT	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-5248b	99	C	T	TTG	TTTAAATTTTC TGGGGTGGT	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-5248a	38	G	C	CTACGTTGT	TTTAAATTTTC TGGGGTGGT	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-4596	69	T	A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-5252	119	A	C	---	---	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-4606	61	A	G	CT	TTAGGTGCTTA AGTTGTCTACT TGG	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-5257	77	C	A	GCAAAGAGG	CCAGGGGCGA TGAAAG	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT
WI-1649	50	C	T	TTCCGAATG	AAAATCCTCCCAATATTG	AGAAAAAGAG AAGAAAGGAA AAA TCTGCTGCTG CTACGTTGT

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTAATTTCTGGAGAGTCAGTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCTAGAACGACAAAGAAAGTATAAGTTGCTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACACCTTCAGTAACGTT
WI-4677	82	T	C	AA	TTTCAACAGTG TCATTATTCAA CTT	AATTGAGATTTTGAACATACGTGACATTTTGGAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCGTTTATAGGGGAATACAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATTTCTGAGAAAAATTTTCACTGGCAATGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTGACGGAAGAAACTTCAA C[G]TTGAGAAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G	A	AACCCACAC G	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTGCCAGTTAGATGACTGCCTCTCCACCGCTAGAAAAAGATGGGAGATTTATTTTC TGCACATATGGAACACACACAC[G[A]CAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTGAGTAAATCAGTTTGTGATGTTGAGATTTTCAAGAAACGTGAAATTTAGTAACCATGGG TCAACTATGAT[C/A]CCAAAAACAGCAGTGTGTCTAAAAATATGATAGTTCTTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	CTGCTCATC GAA	GGTTGGAAACT CAAAATTACCTA GAA	GACTACAGCGCACAGACAGCGCATTTGTGGCTTGCACAGGTGTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCCAGTCCACTTTCACCTGTTTACGTTCCCTGTCTCATCT[C/T]CTAGGTAATTTGAGTTTCCAACC TGTTG
WI-2033	183	T	C	A	CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAGTTTACAGGACCAGTGTGGAAATTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGTAGAACTAATCCCTCA[T/C]GAGAACGTTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGTGGAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCGGCTCTCTCCACCATTTCTCCATCTTCTACTCTGAT[C/G] AGGCAGACTTATATGGAATAAGGGA
WI-2034	150	T	C	CCAAGGAC CC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTCTCGGGTTTCAAGTAAAGACGATGAATCTTCACTCTTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAGT[C/G]GGACCTGCACCTATCTTTACCCCTCCGACACCCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TG TCTTTAAA GTGTGAAGT ATTAATTAG CA	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTCAATCACTCACCATTGCTCTGTTATTGCTCTTCGAGTGT ATCCAAGGATGTCACACTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTTGATA[C/T]TGATGTTCTTTCAAGAGGAAATTTGTGAAGAGGATTCCTCAAT TGCATTTCCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGCTTATTTCTTAGGAAAAAAGTGGTAGGAGAA CACAATTCAGGTTCTCCAGATGCAGAAGATACTAGAAAATGC[C/T]GAACAGAAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATCAGTGCATAGATCATCTTGCTAAGTTCC[A/G] JTGAaaaaaaattatGCCAAAATTTTAAATTTATCCAAACTTTAAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCCTTCATTCT[C/T]TTTGGATTATGAATAGAAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121	G T	TGATAATGGG GCCTGT	CCTTCTTTTA TATGTATGCCA GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC GC	CATATGTATAT TTTCTTCTTG AATAAAT	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTTCCATTTGTTGATTCTTTTGTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATTACAATTTCACTCAACAGGAATTCATTTCTGTAGCAGGT ATA[C/T]GGACTCATTTCTTCTTGCATCTATTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCACATA CCTCATTTATT CA	AAATGAGTAACCCAAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATTCCTTGATACTGAGTAGTGCTT
WI-5328	44	A G	---	---	AACATTTTAAACCATGCTACATTTACAAACACTGAAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAGCTCTTAAGAGATTATGTAATAAAAAAATAATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAAGGAG
WI-4897	93	A G	---	---	GCCTTTTGTAGTTTAAGTCTTTTGTGAGTGTGCTTTTTTTTTCCCCACTAGGTACTCTCGGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCC[G/A]CCTGCTATGTTGCTTGTGGAAGCCACATCCACT GAGGTATATCTGCTGCTATTTCTATATCACTCAGCTTTTCAGATCCACTCCACTCAACTTCAG

WI-5370	143	T C	ATAAAACAA	ATAAGATGG TACCTTAACTA	CAAGTTGGTA CAGAGAAATTC AAA	TGCAATGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGCGCAACATTAACCAAT CTTTTGGAAATTTACCTGTATCCCATCATGGTTCAATTCGAAAAAATAAGATGGTACCTTAACTA ATAAAACAATTCITTTGAAATTCCTGTACCAACTTTGCTTTTC GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAGGAAACACAGAAGAAACGCCTGGTGCAGAGCC CCAAATCCTACTTCATGGATGTGAATGCCAGGTGCCAGGTGAGGAGACGGCTTGTCTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTCGCCTGTGGAAATATTTCCCTGATACTCTTAAAATTTGAATG GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAGGAAACACAGAAGAAACGCCTGGTGCAGAGCC CCAAATCCTACTTCATGGATGTGAATGCCAGGTGCCAGGTGAGGAGACGGCTTGTCTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTCGCCTGTGGAAATATTTCCCTGATACTCTTAAAATTTGAATG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTAAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACCTTAAATGATCTCTGTGGA CTTTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTG TATAGTATTTAACGAAGCCTAGAACGACGGCTGTGGGTGGTGAATTTGGTTC/AJAGCATATCTTAGGT ATATAATAACCTTGAAGCCATAACTTTAACTGGAGTGGTTGATTCTTTTTTAAATTTATTGGGA GGGTTTGGATTTTAACTTTTTTAAATGTTGTTAAATATTAAGTTTTTGTAAAGGAAACCAATCTCTG TGATTACCTCTCAATCTATTGT
WI-9711b	423	T A	---	---	---	AGAATGGTACTTTCATAGGCGAGAGAGCCACTTTTGGCTAATTTTTAACATCCAAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAAACAAAATAAAATATGTCTATTTGGGAATACCTAATAATCAG ATACTAACAAAGTACAGTGAAGATAAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAGC/G,TCCTCTAGGTTAGTAGAAAAAGTT
WI-9711a	390	C A	---	---	---	
WI-9702c	345	G A	---	---	---	
WI-9702b	344	C T	---	---	---	
WI-9702a	179	C T	---	---	---	
TGR- A003N21	49	C A	---	---	---	
TGR- A004V30	203	C T	---	---	---	

TIGR- A004W22	232 C A ---			GGATAAATCAGTACAATAATGGGGACCTTAAACCTGCTGTGATGCAGGAGTGGAGGGCTGGGCAGTG CCGAGGAGGGGAGGACAGTGGGACAAAGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACAGGTTCCACATCATGCACAGCAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATGGTGTCTGCCCCCGCCTAC/AJCTGGAGATGCTCTAAAA
TIGR- A005D24 b	138 C T ---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATCTCTTTGAGATAATTGATTCATATTC TGTGGCTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAATAG/AAAAACCCAA CTC/TJTTTCAACCATTTAGTTTGATTATCATCTGGAATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTACCTTTAATAATTAAGGAAACAAT
TIGR- A005D24 a	123 A G ---			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATCTCTTTGAGATAATTGATTCATATTC TGTGGCTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAATAG/AAAAACCCAA TTTCTCTTCAACCATTTAGTTTGATTATCATCTGGAATTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTACCTTTAATAATTAAGGAAACAAT
U03735	74 C G ---			TGAGTGTGACGAGTGTGACGAGGCGGAGTGGAGGGGCTGGGCCAGTGCACCTTCGGGGGCG GCATCC/CJTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCATCTTCTCACTCTTTGAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTTCTGTTGGATGACTTGAGATTATCTTTGTTCTCTGTTGGA GTGTTCAAATGTTCTTTTAA
U39840b	42 T C ---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAACAAACAA/CJACCACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACAACATTTTATTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56 A C ---			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAACAAACAA/CJACCACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACAACATTTTATTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41 G A CCCC			GTGGCCATCGATCTGGACCGTCCCTGCCACTTGTCCCG/AJTGAGCACTGCGTACAAACATCCA AAAGTTCAACAAACACAGAACTGTGTCTCATGGT
WI-7008	180 A G ---			TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGTAGATGGGTGAGAA AGCACCAGTTCATGATAGGAGTTCAGGTTCATGATGGTACATGGTACCTGATGACCCAGAGTCAACATTCAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGCTCTCAAAAG/AJGAGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGTCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26 C T GGGATCT			GGTCCCACGAATTTGCTGGGGAATCT/CJTGTTTTCCTTAAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGACGGCTCTCTGTTTCTGGTGG

WI-7593	46 G A	TTTTGTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTITTTGGA CACTTCCTCTTGAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G	AGTGCATCTTGGGGAAAGGCTCCAGTGTATCTGGACCAGTTCCTTCATTTTCAGGTGGACTCTT GATCCAGAGA[G/G]ACAAAGCTCCTCAGTGAGCTGTGTATATCAAGACAGAACCCAAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTATATCATAGATAACATCTCCACAGCCTCACTTCATTCAC CTATTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
WI-7059	43 C G ...	GCTCCTCGCTG GGTCA	GCAGAGAAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGTGAATATACCAAATCTGCATCTCCAGAGGAAAAATAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53 A C TT	TCTACTTTCTG OCTTGGGT	AGCAGCCATCAGATGATCTGTTTTTCCACCCTTCACTGAAAGACACCATTTAT[G/C]TACCCCAAGGG CAGAAAGTAGAACCTTACTATTCAATTAATGTTTGACACAAATGGAATTGTC
WI-7079	293 T G	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACCTGCATT CTTTAAAGTTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTCTATTTTCTTTCCATTGCT TATCTTGAGCACAAAATGATAATCAATTATTACATTTATACATCACTTTTGTACTTTTCCAAAGCCC TTTTACAGCTCTGGCATTTTCTCGCTAGGCCCTGGAGGTAACCTGGAT
WI-9074	38 A G AAAAG	GACAGATTTTT GACCTAGTTCC TT	TGGATGCCAGGTAAAGTTCTTTTGTCTAAAGAA[G/G]AAGGAACCTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAAGGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCCTTGACACAGGTGGGGCCACAGCACCCAGCATCTTGCT
WI-7104	157 C A	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGCAOCCAGGTGGGGGCCACAGCACCCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T OCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C/T]TC CTGTCTAGTCTCTCTGTAAGCCCAAGAAATGAACATCCA
WI-9014c	93 T C	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCAAGTATCTTCTGTTCCAGAGAGGTGGGCTGGAT GTCTCCATCCTGCTCAACTTTAT[C/G]TGCACTGAGCTGCAACTTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTTCTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGCACTGAGTGCACCTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTCGGTGCT CAGTGCCTTTAAGTGCATCCGCTGTGCTGACTTGAGTGGGATCAACATCTGCTACGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATCAACAG A/C/A/CACACATCTTCTCTACCCAAAAGCTGTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/C/CCCTGCGT GCTCAGTGCCTTTAAGTGCATCCGCTGTGCTGACTTGAGTGGGATCAACATCTGCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATCAAC CACACACACATCTTCTCTACCCAAAAGCTGTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCTGCTGGCTGGATCCGGGACCCCTTTGCCCTTCCCTCTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAAGCAGAAGAAAGCTGGAGGAAGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTATTATTGTTGCCGCTGTTGTGTTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAAAGTAGAGATAATAATCA[G/A] TCTTTACACCGATGGTAATTAAGCTTGTTATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGAGCCCT ATTCTCTATT ACTG	TCTAGAGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCTCTATTAT/C/CTGCTGCTGCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAATTTAG
WI-7753	52 A G GAAGAACAGA A	CCATGTTCCGA A	CAGAGGCTTG AAATACAGGG A	AAGCCAGATGGACATCCCTGGAAGGACATCCATGTTCCGAGAAGAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCATTTATGAACCTGCCCTGCTCCACAGAACACAGCAATCTCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A CGCA	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGAGCGATGTCCAAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA[G/A]ACCTAGGTGACACTTCCCTTTTCATCTT
WI-9193	94 G A CA	AGAAATTGT CTGCCTTAAAG CA	GGTGTGTGG TAGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGCTGCCTTAAAGCA[G/A]TACCCCTTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATGGGTGGATTG[C/T]GCTTTGGTTAATACAT CTTCCCTAAAGAAAGATAAACACAAAATCCATCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G AGGAGCCAC	GGTCTGAGAG G	GGAGTGGGTGT CATTAGGA	GGAGCCAGGAGACAGCGGTCTGAGAGAGGAGCCAC[G/G]GTCCCTTAATGACACCCCTCTAGCC CTGAGGCTCGTGCCTCTAGACTGGGAAGAGTCCAAAGGAAGGGAGGAGCAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 GC	CAGGTC	CAGTCCCA	CACCTGCCAC ACTCAGAC	GTGACCCGTGAGGTCAGGTCGCCAGATTGA/CJGTCTGAGTGTGGGCAAGTGTGTCAAAGGGGGC TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTGTAGGCGCGAAGAGTCA
WI-7836	120 TC	CAATAAACA ATGCAACGTT	CAGCTCAGCT TAACTGACAG	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCAATTCAGTAGTTACTGAAAGAAACACTCTGCTA GAATGATAAATGTCATGTTGGTCTATAAAGTCCAAATAAACAATGCAACGTTCC/TGJGATTCTTAAT CTTGTTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACACAGCT
WI-7286	65 TC	CTAAGCATGT ACGTGAATTT	CAGCTCAGCT TAACTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCCCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTACAGAGATTC JGTTAAAGCTTTCTGTTAGATTGTTTTCAGTTGGTGATCATGTC/TTCATGTGTACCTGTGTAATAATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 TG	CTAAGCATGT ACGTGAATTT	CCCAATTTTA TTAAAAGTTTA CATCTAT		CAAAATCTTGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACATACTATTACTACT AAGCATGTACGTGAATTTTAAATTT/GJTATAGATGTAACATTTTAATAAAAAATTTGGGTGTGG
WI-7860	50 CG	CGTACCTCCAA ACATAATTGA TTT			GAAGATTAGGGAGGGGTGCTCTGTGGTCTCTCCCTGCCCTCTCCCA/CJA/GTGGGGAGAGACCC TGTAATTTGCCAAGTCCCTGGACCTGGACCCAGCTACTGGCCCTTATGGGTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAAAGAGTCTACTCCAAACCTAGGTCTCTATGTCAGACCCAG ACCTAGGTGCTTCTTAGGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 AG	CGTACCTCCAA ACATAATTGA TTT	GCTTGAGTGA AGTCTGCGAGA		CAAGCGTAGCTCCAAACATAATTGATTG/CJGTATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGGCTGGCTACTGTCTCTGCACTCTGCTGTGG
WI-7307	128 GT	CGTACCTCCAA ACATAATTGA TTT			CACACTGTCTGTCTTTCAGTGTGGAGTCTCTGGCAGGGTCAGGCTGGGGTAAGCGGGGTTCACACA GGGGCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGCGGAGAGCAGTCCCTCCTCAG/GTAACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACTCCTGAAGCCAGCTTGCAACCTCCAGT TTGCACAGGGATTGTCTGGGGCTGAGGGCCCTGTCCCAACCCCGCC
WI-9274	25 CT	GAAATGTGAC TTCACTTGGT	CAGGTAGAATT TTCGTCCATT	G	GAGGAAATGTGACTTCACTTTGGTG/CJCAATGGACAGAAAAATTCACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTTAATAGCTGGTTTACACCTTGATTCGAGGTGGAA
WI-7313e	266 TC				AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAGTTCCTAAAT TGTTTTCAGCTTTTATGTTTATATCATAGGTATAGGTGAGCCTAAATCCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTTTATGTTTAACTTAATCTCTGGAATTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAATGTATAGCGATGA
WI-7313c	256 CT				AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAGTTCCTAAAT TGTTTTCAGCTTTTATGTTTATATCATAGGTATAGGTGAGCCTAAATCCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTTTATGTTTAACTTAATCTCTGGAATTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAATGTATAGCGATGA

WI-7424	131 T	A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGAGGAGCAGAAGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTTCATTCGTCAATCCAAGAGAGAGAGGAAAGAAAA TTATACAACTTTCATTCCTTTCATTCACGTTTCATAAACATTCATACATA
X86400	118 A	C	---	---	TCCTGCAAGAAGTCTCAAGCCTTTTGATTTTGTGCAATAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAAATTTAAGTGAGA[AC]TCTTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAAATTATGTACCACTCGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTCA
WI-8053	242 T	A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGATAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGTCCCATTTAAAGGGACTTTTATCAACCTAA TAAACTCTAATTCGTGCTGACTTTTAAAGATCTAAGGTCAATTTATACATGCTGAAAAAGGCTCACA ATTAATTCCTTTGATCTTTTACTCACTGTTAACTTATATAATTTATTCAGAAC
WI-6190	165 G	A	---	---	TACAAATGAATGTCTTTTATTCGGTATGCATCCACATTTTCAGCATTTAGTGTCTGAAACAGCAAG TGAAAGACGCAGCAATTTGCCAGGAGTCAAGCCCAACCAATTCGGGGATCTGCTGTGCACACCGG GTTCCTCTTAATCCCTGCTGAGGATCTTG[GA]GAAGCAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTGAGATTCCAAACTAGACCCCA
WI-6275	148 G	C	---	---	AACAGTCACCACCAACACATGACAACCTGCCAGGAAGGCTTGTCTCCCTCCCTCCTTTGCGTCCC ATGTGCTTAGTCAGCAAGGTGGGGAGGACCGGATGTAGCTTCGCCCAAGGGAGATTACAGAGA GAGGCTTGGGAAA[GC]GGAAAGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTTCAGTAACTGGTATGCTGAA
WI-6421	41 G	T	---	---	ACCAAGAGATCAGCTGTCTAACACAGCAGCTTTTGTGATTTGTTGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCAGAAA GAATATTGGGGCAGAACCTTGGAACTGGCCACCGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T	A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGTCGGGCTGCTACAAAGGGCGTTCACTTTTCTTCCACCACTATGTACAGTCAGTGCTCAA GGTGATGGGCTACAGTGTGCTGATCAGTGTGCTGTACACACATTTTACATAAATTACACAGACTC ATACATGAAAAATTTAGAGCCTAAGGGCCTGTATTTTATGAGAAAAAAA
WI-9420	202 G	A	---	---	AACCTGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTTGTAAGTCAATGACTGTGTTGTTT TAAAATATGTACCAAGGAAATACAAATTGGATATGATCATTTTTCATGCTCAGGAGAACAGCAC AGAAATAAAGGATACGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTACACAG TG[AG]GCATCTTCTCACCCTTAACCTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A	---			TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGGCTTGTTCCAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A	---	---		ATGTCAGAAGAGACACAGACAAGGAGTTTTCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTOCTTAAAGCCCCAGATTCTCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACAGGGCTCACCTTCCCAG
WI-1245b	201	G T	---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTC/GCCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAATTTCAATTATCATCTGGACAGCCCTTCTTATAAGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C	---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTC/GCCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGGT GGTTTATTAATTTCAATTATCATCTGGACAGCCCTTCTTATAAGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A	---	---		TTCAAGTATAAGGACAGGCTAGAACAAAGCGTTCCCAACCTGGCACCAATGACAGTTTGACCAAA TAACCTTTGTTTCAGGGGACTGTCTTACACATTGTGGGATGTTTAGAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACCAATCATGACAAATGAAATGTCCTTTAGACATT GCCAAATATACCTTGTGGGACAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A	---	---		AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTGAAAGAGG GAAATCTCGATAATTTTAAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G	---	---		ACCAACCGTTGGCAAGGCTCCCCAAGACTCAACACCCAACTTTGTGCTTACCCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGACCCAGCCTAT TGGAAGAAATCATAAATGTAAACCTTACAATGTATTGCTCTGCTGCTGGTGGCCAGGCATAGAGTT/G JGGCCTACAACCCATTTTATCATTGAACCCCTCAGAAGCATCCAGTTGGGCT
WI-5801b	157	G A	---	---		TGTTATTTTCCCTTCCCTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAAGAAATAAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]JAGGGAATGAGAAAAGCACACCAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCTCTTCTCTAAATGTTATGATTAATTAGTGTCTTTGTGAGJGAAATTTGAAAAAATGT AAATCAGAGAACAGAGAAAGAAAAATAAGTAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAAGCACAAACAGAAAAAAGTGTGT GGCTAAGGGAAGCCCAAGGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTAAATCCTGTGCCCAATTGCAAGACTGCATTGAGTCTGATGAGCCTTAGTTTCJCAJTA AAGCCCCCTCACACCGAGGACAATGTTGAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAACTGGGACCAAGATGACTTTATATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGGTGAGTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTATGATAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAAGCTCCTCACCTCCCTTCGAAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGCAGGGACTGTGTCTCTGTTGCCCTGTTGGTCCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCCTTTGGTATACCTTCTCTTCTGAAGACCAACCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGTACTTCTACATCTCGAAACTAGATGAGTAGGCTCTCTTCATCT CAATTGAAATCTAGAAJG/AJAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGCTTTGTGAAGCCACACAGAGATGATCTACTCTTTACJCAJAAAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATTCATTTCCCT TTGTTGAGGAGTTCTTATTGGCCCTTCTTCTAAACCCCTAACCATCTGCTTATTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAACCTCGTTGGCTCAAAGGAAACTGTAGJCAJAAATCTTTTATTTTATTTTGTGTTTTAACTC AAAGAGTGGAGTTGCATTGACCTTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCCTCTAGT GGGCACCTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAAAATGGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGACAAACACTCCAAGAATACJAGJAGATATAAAACATCATCATCA GTAGAGATGGATGACCTAGGAGGTGATGCTGATGAGGCGATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAATAAAC AGTGACTAACTGAGGTAGAGTCAAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATTTCTTGGGACATGCAGAGCAGATACGGGAAGGCATCTTGGGCAATTTGGAAGGAAACGAGCCCTA ATTATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAAGTGGGACAAAGGCTTGTCAJCTCTGTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGTTGAGGAGCTGAAGGCTGAAAGATAGTCTCTGCTGGTCTTTTCGTTGGAATGGATGAGTCCT TTTACAAAATTTTCTCTGGCATGGGTGTTATGTTTGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGCTGTACAGTTTACTGGAAGTTGT/GJTGAACTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAITTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCTCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATACITTAAGTAAATTTTAAATCATGTCATTTAATTA TGCACITTAAGTTGGTACCAGACATTTGCTTCCAATTTGTAATTCCTTAACAACAGCAAGCATAACT GATGTCCATCTTTGTATTCCTAAA[C/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGT CTTCTGTGTTTCCCTTCTGTTTCCCTATTTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACTTCATTTGACATTTCTAAGAGATAAGAAAAACAACGATCCACTGTGTGTTTGCTT GATTT[G/J]GGAGATAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAAATAGCCT TTGTGTGTTGTTTTCAGGAAAGAAAGCCAACTCAACTAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAATCTCCACATAGAGCATTAATATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTCTTTAAGGAGTTTCGGTGC[C/A]AAAATTTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATATTGTTGCTGTGTTCTTGGTG
TGR- A004Z48	177 A G ---	---	CAAATACTCTGCTTAGAAGTTGCTTAGGGCCATGGATTTCATGAAGGTGGGCGAGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGACGGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[G/J]TCTCCAATTTTCAGGGGCTOOC GTGGGATGGTGAGCCCAATGAAGACAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCACT[G/J]CATGACCTCAGCCCCATCTCTTCTCCC TATGTTCCAGAGACAGATAGACCTGGCCCTTCTCTAGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGAGCC TGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT[G/J]AAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTGTTTGTGTTTGGGTATCCTGCCAGTGTGTTTGTAAATAGAGATTGGAGCACTCTGA GTTTACCATTGTAAAGTATAATTTTAAAGTTTGTGTTCTGA

WI-7747a	44	T C ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAAGCTTCAATGCTTGTAAAGTT ATTCTGTTGTTGTTGGTATCCTGCCAGTGTGTTGTTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTTGTAATAAGATATAATATTTTATGTTTGGTTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCACAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCAATTTATTTCCCTTCAAAACAATAATATTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACATTTTTC/JAG TTTGCAATAGAACTAATACTGTTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCGAGCTGGACTCATGGATGTCACCCCTTTGCTCCCTGCTCTTTCTGCCCTGG[G]CTCATGTA TCTGGCAGCTCTGTACCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTGCCCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTTCTTCATCCCATCAOCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]JAGAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCATAATTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATATTGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTTCCGCGCAGTCTTGGGAGCGCTTTGCTGTGGAACACGAGAGCTCCTCT CAGGGGCTGGCAGCTCACTCTATTTCTGTATGATGATGTTTGGTTAAACACTGTCAAAATAAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTTTAAATATTGTAACCTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAATTC/JACAACTTT
WI-7928	101	T G ---	---	CTCCCTCCTATGCTCTCAGCAGCAGTGGGCGCACACTTGTTCATCTTCTGACCCGTTTGGTGGCTA TTCCCTGCAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGGCACTTTAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCCTCATTAAAAAATACGTACATTTCCGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAAAGACTTAAAGGGCCCAATGAATTTATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCACATATAGACACATACACCAACACTTACACCAAACT[A] ACTGAATGAAGAAGTATTTGGTAACCAAGGCCATTTTGGTGGAAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGGTTCCAGCCGTTGCCCACTCATCTGCCGCTTGTCTTGTGGGGGAGAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATGTC/JAGCCCAAGTACAGCCTGGACCACCCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCATGGGACAGTTACACTTGGACAGA CAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	---	TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATATTTTCATACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGT[AG]GTGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTCAATTGTGGAATAGTTTAAACAGTCAAGGCTAAACCTGGTCAGTATTAAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAAATGAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCAGAGAGATTAGCAACAAGGATTCACTCTGTACTACTTGCCCTTTTATCTTTCCCTCTTGCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGCCAGTGT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATGGCAAAIGICATCAG
WI-140	252 C T ---	---	---	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAATAGATTTCATTTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTACGCCAGCTCAATTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTTGCTGTATTGGCATTCCT[C/
WI-198	218 C T ---	---	---	GAGGTCTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTGTGGCACCC CATGATGGAACCTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTACGCTA CCTGCTTCCCTT[C/TT]GTTTAAACAAGCATAGAATATTCGAACAAC
WI-205c	146 T C ---	---	---	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/CC]AAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/CC]AAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNTTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCCCT CTCCCCCACAACACACAATAACAGAGATT[G/C]AATTACAGGAGCCAGTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTAGTTTCTCAAAATGGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAACCAACAT[AG/C]TTGACTCTCTTATCTCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCTGAACGGAGGAGGATGGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCCTCTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---			AGCTTTGAAATCCAAAAACCACATAGCTTGAAGCTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAAATACAGAACACCCCTGTGGCTGCCTGAACGAGGAGGATGGGCGGGGAGACAT CGGTCAATGATATCAAGCATCTCTGCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAGGGCTTGTCTATCCTCTCTGCTATCCTGATGACTGGGCAA
WI-427	59 G A ---			TTTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAATTTAGAACTACTTCC[G/A]GTTT TTTCCCTGGGAAATATTACAAAACATTTGTGGCTGCAATCAGGTTAAAGACATAGTGGCCA TTTGTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGTACCAGTGTGAGACTTTATGT ATTCAATTTATTAGAGCAGGGTCTTGTCTGTGCAACCCAGCTTCAGTGCAGT
WI-562c	106 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAITCJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAITCJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAITCJAAATAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---			TTCAAAATTAACACCAATTGGGTATATTATAATTTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCTTGAAGTATTACGTAATCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCTCACCCCTACTTGGCTCTGACTTCTCTTCTCTGGCT GAACCTTCTCTGTGGCTGTCCGCTTCTCTGCTTGGCTCCAATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGCTTTATCTTAAATGCTGGTGCAGTATCTACCCCTTA GGGATAATTGTGAGAAATCAATAAGTTACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGCTTTATCTTAAATGCTGGTGCAGTATCTACCCCTTA GGGATAATTGTGAGAAATCAATAAGTTACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATGTCAGA CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGATATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAATAATATCTCCCCAGGACGCTCTTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCCCCACAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGATATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAATAATATCTCCCCAGGACGCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCCCCACAAGCACACATTAGAACTTA
WI-867	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGATATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAATAATATCTCCCCAGGACGCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCCCCACAAGCACACATTAGAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCACAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTGTAATGCAGCTGTTATGGCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCACAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCACCTACCTCATGJGJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTGTAATGCAGCTGTTATGGCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTTGGTNGTGGAGAAATCCATTTTGGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATAIT/CJG ATCCGCGATGCAACATTTATTAGTGAAACATGATGAAATGAACATAAT
WI-921b	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCCTCAGCGCTGCCCGCCCAAGAAAGTCTNGCCAGGAAAGACGATCCATCTAC TCT/GA/GGGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-921	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCCTCAGCGCTGCCCGCCCAAGAAAGTCTNGCCAGGAAAGACGATCCATCTAC TCT/GA/GGGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNATTGGCTAAC/G/CJCATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNATTGGCTAAC/G/CJCATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAGAAGTTCCTGCTCAGGAAGTTATTCATTCAAGCAACCTAAATTTGTTTTGAGTACAT ATCAAGCACAGGGTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCT/CJCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAGAAGTTCCTGCTCAGGAAGTTATTCATTCAAGCAACCTAAATTTGTTTTGAGTACAT ATCAAGCACAGGGTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATG/AJTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTGCTTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTCTGTTCTG CTTCTTAAAGATACAAAATAAATGTAAACATTAGACCTCTCACTA/CJGCTGTTTTTACTCTCCTCTG ATTTTTTCCATTATTTTATTGCTCTGGCTTCAATTTGTAAATNTG

WI-1147b	204	G A ---	---	TTTGCCATTATTGAAGATAACCCACACCTGGTGTCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAAACTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTACCATAAATCACTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147	C T ---	---	GCATTGAGAGGGTTCGTTTAATGACATTCAGTGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTCTGGGG/C/TTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G ---	---	GCATTGAGAGGGTTCGTTTAATGACATTCAGTGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C ---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACATTAATCCCTAGACAGCCATTCTTTTGAATGN/C/GNCANT AAAAATGATTGAAATTGGGAATAAAGCCCTCCCTCTAATGATTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202	C T ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNNTA TGAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/C/JTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNNTA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/C/JTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNNTA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNNTA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTTCTGCATTGGAATAGTTGACITTCATGAGNNNGCAATAAATGGACAATCTTGNGNNNNNG GGCTGGGTGACTGTCCCTGGTCAITTAGAAGCCATAGAGATGAAAGTAGCCGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTACCTAAGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTTAA/GJGC
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACITTCATGAGNNNGCAATAAATGGACAATCTTGNGNNNNNG GGCTGGGTGACTGTCCCTGGTCAITTAGAAGCCATAGAGATGAAAGTAGCCGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTACCTAAGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJCTTCCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACITTCCTCTCACITTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTCTT CCTACCCCTCTAAATGTATCTTNTCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGCTGTGTTTCTCTCTCTGTAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACITTCCTCTCACITTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTCTT CCTACCCCTCTAAATGTATCTTNTCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGCTGTGTTTCTCTCTCTGTAAGNTGTTT
WI-1325b	169 T C ---	---	GAGAGATGCCAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTT/CJACCCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCTCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGCCAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTT/CJTTCTACCCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCTCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAGTCCTGTTATTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAAGTTGGTAGCTACCAGGCTCCCAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAGTCCTGTTATTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGTAG/CJGTACCAGGCTCCCAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136	G A ---	---	TATCAGCATGATTGGCGTGTGGACACAAAAGTCAATTTGTACATTTTGTGNTGNNNTCCTTTCTTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNTTAAATTAACCCCAAGC [G/A]GGATTGTGATGGATGTTATTTCTGTGCTTGGAAACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCAGGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGTAGGTGTCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAAATGTGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGTAGGTGTCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAAATA ATTTGAGAAAATATGATAGAAAATGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGTAGGTGTCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAAATGTGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGTAGGTGTCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAAATA ATTTGAGAAAATATGATAGAAAATGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGTAGGTGTCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAAATA ATTTGAGAAAATATGATAGAAAATGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57	C T ---	---	TGGTATTTGGAATGGGTTCCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACGT AAAGTTTACATCAACATAAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58	T C ---	---	TGGTATTTGGAATGGGTTCCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCT[C/T]TCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACG TAAAGTTTACATCAACATAAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCCTC ATAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---	---			CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCAAGAGAAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTAAGGGCTCGGCTTCAAAAGCTGGGTCCGGTTTGAGGGGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTTGC/TTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---			CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCAAGAGAAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTAAGGGCTCGGCTTCAAAAGCTGGGTCCGGTTTGAGGGGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTTGC/TTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---			CCATGAGCAACAGCATGTTCTACTCTGTGATGTGATGTTAGGGGCGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTCCGTGGTACCTTCTCTCCACCATCACCTGTGTTTT
WI-1732b	122 T C ---	---			TGCCTACTTCTTTGTTCAATCCACCATACATTTTGTAAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCTTTT/CJATTCAGTCT CTGCCACATGCTAGTAAGTGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T ---	---			TGCCTACTTCTTTGTTCAATCCACCATACATTTTGTAAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCTTTTATTCAGTCT CTGCCACATGCTAGTAAGTGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G ---	---			GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTTAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG[A/G]TTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTCCTGACTGAG CTACATTCACCTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---			GGTACACAAAGAAATGCTTCTGGAAATCTAC/A/GTAGCGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAATGAAGCTGGGAAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAACTGTAGAACAAATAATTCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGAAATATCATAAAAAT
WI-1803c	77 A G ---	---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTINAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTACTTGTGCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATGAGTAGGTAGAGCATCACACTTGGGAGGACATAATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTTCOCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACIC/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACAACCTGGGAAGTCTGGGAACGTTTTCGCTTTCGCTGGCT
WI-1837	112 C T ---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTTCOCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACIC/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACAACCTGGGAAGTCTGGGAACGTTTTCGCTTTCGCTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGTGTGAGAACTCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGTGTGAGAACTCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCACTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/TTCGTGCAAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879	110 C T ---	---	GGGCTCACTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/TTCGTGCAAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCTGTGCTGTGAGAGGT AAAGTGCCCTGCCCAACCGGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAACTGCCATGAGAAACCACTTTTCTTTGCTCC

WI-1900	119	C T ---				TGTTCTCTGGTCCAGGCCCGGGCTAAGTCTTGTCGTAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGGGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAACTCGCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C T ---				ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCAATCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165	C T ---				ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCAATCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164	C T ---				ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCAATCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270	A T ---				CCAGGTGAGGCTGAAAGAAAGGAGGAGCAATTGCTGTGGAGTGAGGATCTCGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGCTGAAAACTTAAAAATGCACCTCCCACCTTT
WI-1960b	270	A T ---				CCAGGTGAGGCTGAAAGAAAGGAGGAGCAATTGCTGTGGAGTGAGGATCTCGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGCTGAAAACTTAAAAATGCACCTCCCACCTTT
WI-1977	203	T C ---				CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGATCA TTCTGGGCATTTCTTCATAGAGTNTTTTGTAGTCTCGTAATAATACTGTGCCCTAGGAAGGTTGTT TTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATT[T/ C]TAACAATCAACACACTGGCTGAGGCTGTTGG
WI-2012	102	T C ---				AAATCTAGAAGCCAGAGTCAGCTCAGCATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAACCTAGCTAAAAAT[C/T]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACCTTTTTTCTACTCTCATT GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T ---				CTTTAGAGGTGGTCATTTGGGTTCCCTTCTGGAAGTATTGTTTAAAGAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAATAGTGTACTGACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACITTTGTTGAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---				ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTACTACTCATATATTGCTAGGATATCCACATACCAAAAGCCAAACCTTAACC ACATACCCCAACTGGTTTCTAGATGTACACG/AJGTGGGACCTCTGTCTCAACCTCCGACTTTTAC AGATCATGGTTAGGCTCACCTTCTGTAAATTGCTCTGTTTTCAAAAGGG
WI-2032b	219 C G ---				ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTACTACTCATATATTGCTAGGATATCCACATACCAAAAGCCAAACCTTAACC ACATACCCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTACAGA TCATTGGTTAGGCTCA/C/GJCTTCTGTAAATTGCTCTGTTTTCAAAAGGG
WI-2032	219 C G ---				ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTACTACTCATATATTGCTAGGATATCCACATACCAAAAGCCAAACCTTAACC ACATACCCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTACAGA TCATTGGTTAGGCTCA/C/GJCTTCTGTAAATTGCTCTGTTTTCAAAAGGG
WI-2054b	188 C T ---				CGTTTCTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTCTC/TJCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTTT
WI-2054	183 T C ---				CGTTTCTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTCTC/TJCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C ---				TGGGATTAAACCCCTGTTTCTTCTTCCAGTTCAGTGTGCCCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGTCTTAAATGCACCTTCCCGTTACAAGGTGTTTCCGTGCTTTTGTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAGGTTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---				TGGGATTAAACCCCTGTTTCTTCTTCCAGTTCAGTGTGCCCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGTCTTAAATGCACCTTCCCGTTACAAGGTGTTTCCGTGCTTTTGTATAT CATCTGATCTTCCCAACAGGGCTTATTTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT TGAAGTGAATGATTTGCTTGCACAGGTTCATATGGCTGGGCTTGGACGAG

WI-2573d	129	T C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTT/CJ/GA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTGATAT CATCTGATCTTCCCAACAGGGCTTATTT/CJ/GCCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTTGATAT CATCTGATCTTCCCAACAGGGCTTATTT/CJ/GCCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T C ---	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTTT/CJ/GA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGAACAAAGCTTTCC/A/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAAGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGAACAAAGCTTTCC/A/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAAGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTTGCTGCTGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA/T/CJ AGAAATGAATAGAGCCCCATTTAAATTATATACAGCTTTATGTCCACTTCTGCTTCTGOCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTTGCTGCTGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA/T/CJ AGAAATGAATAGAGCCCCATTTAAATTATATACAGCTTTATGTCCACTTCTGCTTCTGOCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACACATATCTGTTGGGACITTAACAGAGCAAGGCATAAAAAT/TAJGACGACCTGGGGCA CAGAGGGAGCTCTATGCATTNATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTTGGGACITTAACAGAGCAAGGC/AGTAAAAATCAGGACCTGGGGCA CAGAGGGAGCTCTATGCATTNATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACACATATCTGTTGGGACITTAACAGAGCAAGGC/ATGATAAAAATCAGGACCTGGGGCA CAGAGGGAGCTCTATGCATTNATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCAGCATTTCTAAGAT/TC/G CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTCTTAATAAACCTAAC ATTCTCTTTGTTCCCTGACATTCGAAAGGACGCTGCTAGATGTATGCCAGATTGCCAATCCT AGTTCITTAATGTTATTCTGAAGAAACCTTTTACTAGGGATTTGCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCAGCATTTCTAAGAT/TC/G CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTCTTAATAAACCTAAC ATTCTCTTTGTTCCCTGACATTCGAAAGGACGCTGCTAGATGTATGCCAGATTGCCAATCCT AGTTCITTAATGTTATTCTGAAGAAACCTTTTACTAGGGATTTGCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TAATCTTTCTTTCTGGT/TAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA AATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TAATCTTTCTTTCTGGT/TAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	GC ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	AT ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	GC ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995b	151	GC ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995a	133	AT ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-3147	85	CT ---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCCAC ATCTCAGTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTTCCCTACTCTCTATCTCCTGAGACTTCTTCCT GAATGAATTAGATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTCAGGAACTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTGCAAGG
WI-3234b	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAAGCAAGAACAAACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGGAATGTACTTATTTTATATCTTAT
WI-3234	68	TT C ---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAAGCAAGAACAAACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A ---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGAGTGGATGGGATGGATTA GCCATGAATATTTCCATTGTTTCTCATTAATGATTAATTAATTAAGTAAATATTTTNCATGA GACACATGGAAAAATGAAACATTCATGGAAAAAACCCATTCAATC
WI-3292	106	G A ---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGAGTGGATGGGATGGATTA GCCATGAATATTTCCATTGTTTCTCATTAATGATTAATTAATTAAGTAAATATTTTNCATGA GACACATGGAAAAATGAAACATTCATGGAAAAAACCCATTCAATC
WI-3355	19	G C ---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTTACTGGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATCTATCCCTCCAGCACTTAAACTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATACCTTCACCTTTCAATGGAAAACTTTATAA ACTGGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTINAGTIG
WI-3408	194	G A ---	---	CCATGAAGAATGAGTTCTCCCTCCCTGGTCACGCTAAGAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACACCTTTATGCTTCNAAGCTTT CTGGAATGGGATGAATCTNACATCAATGTGCACCCCTCGTGGGATCACTTCTCC[G/A]TGCCCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG
WI-3505b	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCATTGTGCATCAGTGCACCTTAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTCCTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3505	131	G A ---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCATTGTGCATCAGTGCACCTTAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTCCTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3564b	177	C T ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTGCTAAATGTTTGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTACATGGCAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[C/T]AACAAAGTGTGTTGTTGTCATC AGTGTACACATGCTACCTTCCCTTCACAAAAACAA
WI-3564	177	C T ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTGCTAAATGTTTGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTACATGGCAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[C/T]AACAAAGTGTGTTGTTGTCATC AGTGTACACATGCTACCTTCCCTTCACAAAAACAA

WI-4110	130	T C	---			GAAAAATGATGTTTGGATTTCCCTTCTCTAGATTATTGGAGTGTCAATTAGAAAACCTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCTCTCTCTCTTATTTTGCCT/CJACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAGGGAGGAGGTTTCTGGGAAGA
WI-4119b	168	G A	---			ACCTCTATGCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAGACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G A	---			ACCTCTATGCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGGACAAGACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T G	---			CAAAGTCAGATTTTGAATTTTCAGGATAACAATTTGAAAATAGAAAAGTG/GTJTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATCTCTCGTTACATAATGTATAGAATTTAGTGGG TTCTCCATGACATGGCTTGTCTCTCTCAACAGTGGGTGGATGTTTCCATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G	---			CAAAGTCAGATTTTGAATTTTCAGGATAACAATTTGAAAATAGAAAAGTG/GTJTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATCTCTCGTTACATAATGTATAGAATTTAGTGGG TTCTCCATGACATGGCTTGTCTCTCTCAACAGTGGGTGGATGTTTCCATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C	---			TTGTACATGTTTCATCCCTCCCTCCCTCTTTCTGTCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4149a	137	T C	---			TTGTACATGTTTCATCCCTCCCTCCCTCTTTCTGTCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC T/C]GTGCTGTGCCCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCCATGATATAAGGTAATTG
WI-4182	188	G A	---			TAAACACTTTTTCATTTGGTTTCTTCTTACTGCAGTTAAAGGACCATCCATTATATACAATTCCTC AGTTCTATGCTTTAGAGTNCATATATAGGACTACTGTAAATTTACAGAGGAAATTTACTCCTTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTCTTAAATTCCTAG

WI-4230	93 T	---			AGAGACGTTGAATGGGACATCTTTCTATTTCGATTTAGTTTAAACATTTGATAAGAAATGATGAAA GTTTGTCACATTCAGATTTATCTTTATAGCAGCAGAAAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAAAGATTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTCGAAT ACATTTTAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C	---			GAAATTCATTTGAAGTTTGACCTTGAACTGATCTCATTAATACTTTTNCCTTGAGTGGTTGTATTT CATTTTGACAACAGAACAGACGAAAAATTTCCACTTAAAAATTAATTTCTC/TJAAGTATCTATGAT TTAGCACTGTTAGCACCCAGAAACTGTGAAATTAATCTCCTAGATATCTTCAGAATCTAGGATGGAAG AA
WI-4271b	151 A	---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCCCTTTGTCTCAGG CTCTTAGAAGTCCAGTCAGGGGC
WI-4271	151 A	---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCCCTTTGTCTCAGG CTCTTAGAAGTCCAGTCAGGGGC
WI-4389b	156 G	A ---			AATCGAAACATTGATTTTGTAAAGGAACACATTATTTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATAACCTTTTGGGA AGGTAAGATGTGAACCTATACA/G/ATJNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAAGCGGTAA
WI-4389	156 G	A ---			AATCGAAACATTGATTTTGTAAAGGAACACATTATTTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATAACCTTTTGGGA AGGTAAGATGTGAACCTATACA/G/ATJNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAAGCGGTAA
WI-4488	31 A	G ---			GATGACAATATTGIGTATTGGCATTTTAAJ/G/GTACCATTCATTTTCTTCTGGCTTTCGTGTGTT TGTTGTTGAGAAAGTCAGGGGTAGTCGTATTGCTCCTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G	C ---			ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAACCT GTCTTGACATTTGAAAAATAAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG/G/C/GTITTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACGTCA TTTCTGTGCCATAAAATAAAATTTTACATGCGCT

WI-4584	144	A G ---			TTGGTTGGCATTAGCCTCATAACAATAATTACAATCAATGTTACTCTTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCAGATTGAAGCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAAATGTTAATTAATTAATGATGCGATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAAAATAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T ---			TTTGTCAATTTGAATGTGATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAITCCACCATTTAC TGACCATATGACTTGGGAAACATTATCTCACCTATCTGAGTCTGATCC[C/TT]CATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAAATGAAATAA
WI-5327	63	A ---			AAATGAATCCGCTTTAGAGCAAAATACCAAGGCTGGTGCAGGATGGTGGTGGCTGAGAGA[A/-] JGATTACTCATAAAAGCATATTAAATTTATAAATATGAAAAATTTAACTAGATAATTAATGTAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGAGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACATGATGAATGTTCTTAAGCAGACAG
WI-5390	87	C T ---			GCTTTTGAGAAATGAAAGGGGAGCCTGGACCATTCGAGGGCTTCTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTATTC/TTGCTCTGCTCCCTTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCAGTGCCTGGCCGATTCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAATTG ACGAATGGGTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---			CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGCAAGAAATCAATTAATAGCAGT GCAACATTATTTAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGTTTAGAGTTTCATAACAA
WI-5404	87	G A ---			CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGCAAGAAATCAATTAATAGCAGT GCAACATTATTTAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGTTTAGAGTTTCATAACAA
WI-5545b	77	A C ---			TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTCCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATGCGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTICA
WI-5545	77	A C ---			TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTCCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATGCGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTICA

WI-5860b	134 A G ---	---	---	ACTCAAGTTTGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTCTTACTCCCTAACCAACCTTCTAACTGAGGAACACTAC[A/ G]TTACTGGAATCATGTGAAGACATTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTTGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTCTTACTCCCTAACCAACCTTCTAACTGAGGAACACTAC[A/ G]TTACTGGAATCATGTGAAGACATTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCCTAACCAATAC TATATATTGCTCTGTTCTGAATTTATTTTCAATTTAGAACTGTAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATTTC/G]TAGTAGGTACCCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGCGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCT[C/ AAACCTATATTNCTGCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGCGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTAA ACCCTATATTNCTGTC/C]CTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGCGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTAA ACCCTATATTNCTGTC/C]CTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTGCGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCT[C/ AAACCTATATTNCTGCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCCTATCACCTCCATCATGCTGCATAACTGATTGATTCAATAATGCTTATTGTTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGAT/C]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103	T C	---	---	TAATTGCACAACTACATATCAGGGTTCTGATTGAAAGGAGAGAAATATTCCTTTCTTTAGTGATT GCTTAATATTAAATCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGAAGACTT CCTATTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T	---	---	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTCTCTACTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAGAGCTGGACAAACCTGCTTCTTTGCAGAAAGAGTCG GGTTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGTCTTGGTAGAGCCCTCTTGGAGACACTGACAGT
WI-6336	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATACTCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGTCTTGGTAGAGCCCTCTTGGAGACACTGACAGT
WI-6381	92	C A	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTTAACAACTAAGTATTTAAAGCTCAAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCCACCATGGCTTTTGAATGTCTCCTCACTCCCAACTTCAACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTACAG
WI-6436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAATACAGGCTTAGGAAGACAGTAGTCTCTGTGTTGAA ATTTGGTGTCAATAAAGAAAGTTAGACTTTGGTGGTTGAGTAGTTGAGTAGTAGGTAGCGTTCTA GJATTGGGTGATTCACAGACAAAGGTGATGTTCTAAGATTGATAATTTATTGT
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTATCATCTGCATCTCTGATCTATGCTGGCTCTATTCTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTAAATTTTCTGTGGGTGATTTATA
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTATCATCTGCATCTCTGATCTATGCTGGCTCTATTCTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTAAATTTTCTGTGGGTGATTTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[T/C]TGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAGTCCCCAATTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTAAATTAACCTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTAAATTAACCTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTTAAAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCCCTACCAATGTGACTCTTTACCCAGGCCCTGTTCTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCCCTACCAATGTGACTCTTTACCCAGGCCCTGTTCTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCCAGAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCCCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCCAGAAAAGGAA AGC
WI-6666	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAGGTTATTTATACCTCTACTTTTCCAAAACAGAGAAACCTCCCC A[C/A]AATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTACTCTGTGTTTTCATGTAA ATGTTGGGGTGACTCATTCGCGCTCTCTNITCTCAAGTCCAGGCTTCTTGGGTAGACCAAACTA ATACAAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G	---	---	AGATTAAACATAATTATCTAGTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGCGCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTTTAGAAAGGGAT
WI-6670	120 A G	---	---	AGATTAAACATAATTATCTAGTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATCTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGCGCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTTTAGAAAGGGAT
WI-6704c	33 T C	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAAATCGATTCTTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAAATCGATTCTTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAACT[C/C]AACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAAATCGATTCTTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	G A ---	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGAAATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTACGGCTGGAATGATTCCC[G/A]TGTAAACTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTTACTAGTCGACACAGGATGTCAACAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	G C ---	---	---	AAAACAAATGGTGCAATTGCAATAATTTGGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCCAGTTCCTCTCTC
WI-6766	148	G C ---	---	---	AAAACAAATGGTGCAATTGCAATAATTTGGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCCAGTTCCTCTCTC
WI-6787b	97	A G ---	---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAAATTTACAGTCTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTCAATAGGGCAGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105	C G ---	---	---	GAACCCACAGGTCCTGTTATTTTATTAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGGCTCTCAAAATCAATCAGTCAACCCCTC[G/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGAAAGGGGAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTCTCATCACAGGTAATAAGGCAAC
WI-6810b	37	T C ---	---	---	CACAATAATAAAATCACTCCCTACCTACCTGAAAACCTTTAT[C/J]AGAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTAAATGCTATGNACAAGTACAATTTCTTTTGTGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T C ---	---	---	CACAATAATAAAATCACTCCCTACCTGAAAACCTTTAT[C/J]AGAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTAAATGCTATGNACAAGTACAATTTCTTTTGTGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C A ---	---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTGTTCTAGTA TTTGTCTTTTGTATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAA[C/J]ATGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCTGTGAG

WI-6817	145 C A ---	---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAAACATCATCACTAACTCAACAATGTAGCT GCAGGTAAC[C/A]TGTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTGTTCAAAATCTGGTTGAGGTGGGCTGTGCAG
WI-6819b	221 C ---	---	---	GATGGAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTCGACTTTTACACAGCGAGGAGCCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G/T]CATATACAAAAATTTCTGCTATTTG CTTAGCAACACAGCAATAAGTTTGGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 GT ---	---	---	GATGGAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTCGACTTTTACACAGCGAGGAGCCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G/T]CATATACAAAAATTTCTGCTATT TTGCTTTAGCAACACAGCAATAAATTTTGGTTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	---	GCAAAAGCTTTATGGCTCCAAACAAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGATATG/GAGCTTAAATATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6826	154 A G ---	---	---	GCAAAAGCTTTATGGCTCCAAACAAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGATATG/GAGCTTAAATATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6857a	122 TC ---	---	---	AGTGCAAACTATTTGAACAAAAGTAAACATATGAGTCACAGCATTTACGAAGACATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAATACAGCAGATGAGATGTCTCTACATGTAT/CJATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAGTGTAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153 G A ---	---	---	TTATAGAATCTTATGGGGCATACNGTAAATGAACGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGCTCTGAAATCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAAACTTC[G/A]TAGAGCCATTTGTGCAGAGAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGCTGTTAGAACTGAGCTCATTA
WI-6909	73 C T ---	---	---	ATTGAAAACTGGTTAGCAACAGATAAATTACATATAGAGCTGGATATAAAATGAGAGAAGATGC AGACTT[C/T]AAGCTTATAGAGAAAAGTCAAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATATTTTCGAATAATAAATCTGCCAGTGCCAAATCAG AAACACCATTTCCACAATATTTGTCATGCCCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163	G T ---	---	CACTCAAAACCTTTATTCAATTGATTTACAAACGTGTACAATATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGCTTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTACACTTAAGCCATTACCAATA/GTJTGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCGGACCTTCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A ---	---	GCCTGTTTTTTGTTTTTTTAAAGTGACACCTTGGCTTGTGGCAATTTCTTCACCTTATCTTACCC AAAAGTGCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGTGGTTTTAAACAATGTGGT CGTGTGAATCAGGTGATTTTCTATTTGGTAGTATTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C ---	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTCTTCGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATGAGAGTTTCACTCTTAATTTTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTTC/AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C ---	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTCTTCGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATGAGAGTTTCACTCTTAATTTTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTTC/AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A ---	---	TTTTATGAACATTTCAGATTCCTCATATCACAGCACATCAATAGCAGTATGTACATAGACTGA CTTTATAGTACG/AJNGTCATGTCCCAAATTCCTAGTAAAGTATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	G A ---	---	TTTTATGAACATTTCAGATTCCTCATATCACAGCACATCAATAGCAGTATGTACATAGACTGA CTTTATAGTACG/AJNGTCATGTCCCAAATTCCTAGTAAAGTATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47	C G ---	---	AAACTAAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAATC/GITTTCAATTACATTAGG AAATCGGTGGATAACGGAGTAGTATTCCACTTAAGAAGCATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAATGGATTTGAAACCACCTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T ---	---	ACTTCTAGTGCCTCTGTTACCACACCTCTAATGCCTCTGGTCGCCGACCTCTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCTCTGTCTTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCOCTGTCTGACT CTCTCCTGATGTTGGGCCCTCTGTGCTCTCTCTCCG/TJGTCGGATC

WI-6996b	242	G T ---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTGGCCGCACTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCGCGCAGTTCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGCTCTCTCTTCQ/GTJGCGGATC
WI-6996	228	T G ---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTGGCCGCACTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGCGCGCAGTTCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTG/TG/GTCTCTCTCTCCGGTCCGATC
WI-7021b	112	G A ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCCTGAAAGCCACAGACAATATGGTCCCAAT/GA/CCTGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCCTGAAAGCCACAGACAATATGGTCCCAAT/GA/CCTGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---	---	GGCAGTAGGACACAGTGTGGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGAC/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T ---	---	GGCAGTAGGACACAGTGTGGGGTTCTGCTGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGAC/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C ---	---	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACGCTCTATAAATAGTATTCGAATCACTGTG CTTAATTTAAATAGCATT/CJCTTATCATTTATCAGCCTTTATGATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C ---	---	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACGCTCTATAAATAGTATTCGAATCACTGTG CTTAATTTAAATAGCATT/CJCTTATCATTTATCAGCCTTTATGATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7175	194	C T ---	---	---	CTCCTAGACTAGTGCCTTACCTTTATTAACTGTGACAGGAAGCCCAAGGCAGTGTCTCCTACCA ATAACTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATAATGGTTTACTGCTGTCATTGTCCATGCTA[C/T]AGAT AATTTATTTGTATTTTGAATAAAAACATTTGTACATTCTGATACCTGGG
WI-7178b	273	G A ---	---	---	TGTATCAGGTGAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCTAGGGGAACAGACAGTACCCAGAAAGCATACACCA ATCCAGGGCTGGCTCTGCACTAAGAGAAATTCACATAATGAATCTCGTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCAAAGCCAGTGAATGTGAAGGA
WI-7178	273	G A ---	---	---	TGTATCAGGTGAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCTAGGGGAACAGACAGTACCCAGAAAGCATACACCA ATCCAGGGCTGGCTCTGCACTAAGAGAAATTCACATAATGAATCTCGTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCAAAGCCAGTGAATGTGAAGGA
WI-7182b	116	A C ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCACTCTGAGCCTA/C/TCTCTCCTCTATTT TACTTGAGGCTGCCAATTAACAGCCCAAGTTTTCAGCTCAAGAGATGCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAAT
WI-7182	106	C A ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCCA/C/A/TCTGAGCCTATCTCCTCCTATTT TACTTGAGGCTGCCAATTAACAGCCCAAGTTTTCAGCTCAAGAGATGCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAAT
WI-7191b	273	T A ---	---	---	ATAATTGCTGTTTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCACAGCACCACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAAATGTGTACCTATTAAATTTGAATCAGCAAGTAGAAGACCAATTT
WI-7199c	112	T C ---	---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGT/C/GGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCTTAATGTTTGTGTTGGTGTCTGAATTTCTTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCATCTTGCTAA
WI-7199b	112	T C ---	---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGT/C/GGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCTTAATGTTTGTGTTGGTGTCTGAATTTCTTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCATCTTGCTAA

WI-7216c	237 T C ---				TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATCTCAAGATCCCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTCTATACATAGGAAAGACACACATCCACCTAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTGTTTTCCTTGTATCATT
WI-7216b	237 T C ---				TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATCTCAAGATCCCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTCTATACATAGGAAAGACACACATCCACCTAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTGTTTTCCTTGTATCATT
WI-7220b	147 A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATTTATGTCTCTTTAAGCTGGCAAAACCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAACACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7220	140 A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATTTATGTCTCTTTAAGCTGGCAAAACCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATCTTGAACACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7226	232 C ---				GATCGAATTTTCAGATGATCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATGTATA TACATATCACCTCTCTTAAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTATCATTT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTAACGATTCCTCAGTCTTGGGGTTT
WI-7228b	254 G A ---				ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCCAATTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTCTTGTCTTGTAACTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAAATGTTATCCAACCTATTAAGATATCTCAATGT
WI-7228a	163 G A ---				ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCCAATTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTCTTGTCTTGTAACTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAGATGAGTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAAATGTTATCCAACCTATTAAGATATCTCAA
WI-7233c	213 C T ---				CGATCGTACTGOCAGTAGCATTGTCTGTCTGCGGCTGTTGTGTACATTTTCAATTTGTACATA GATGTGAACTTTATCTCTGTCATAAATATAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTGCCCACCTTTTGTGGCAATATTAAGTGAAGTGTCTAATA GTGTAAGTATCTGTGCACAAAACCACTGCCAGATAACCAAGAGGGCCCTG

WI-7233b	213	C T ---	---		CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCCGGCTTTGTTGTACATTCATTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACTAATTATATTAAATATTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTATCTGTGTCACAAACCACTGCCAGATAACAGAGGGGCTG
WI-7233	211	T C ---	---		CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCCGGCTTTGTTGTACATTCATTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACTAATTATATTAAATATTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGT/CJACGTGCACAAACCACTGCCAGATAACAGAGGGGCTG
WI-7238	128	T C ---	---		GGGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACATTTTGTCTTAGTCTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGCTTATGTTTCAAGTTGTTTT/CJCCGTT CTGTTTAAACAGAAATAAAAGGAGTGAAGCTCTTTCTCATTTCAAAGTTGCTACCAAGTGTAT GCAGTAATTAGAACAAAGAAAGAACATTCAAGTAGAACATTTATTGCCTA
WI-7252f	520	T C ---	---		CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCGAGCCCGCCCTGGCTCGGAGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCTCTCCA
WI-7252e	552	T C ---	---		CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCGAGCCCGCCCTGGCTCGGAGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCTCTCCA
WI-7252d	540	T C ---	---		CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCGAGCCCGCCCTGGCTCGGAGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCTCTCCA
WI-7252c	552	T C ---	---		CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCGAGCCCGCCCTGGCTCGGAGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCTCTCCA
WI-7252b	540	T C ---	---		CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCGAGCCCGCCCTGGCTCGGAGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCCTCTCTCCA

WI-7252a	520 T C ---			CCACAGGATCCAGCCCAAGGGCCCTCCGCCCCCTCCACTCGCAGACAGCCGGGACAGAG GCCTGCCGGGGCCAGCCCGCCGCGCTGGCTGGAGCTGCCCCCGCCCTGGTCTCGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCCTGCGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA
WI-7265m	252 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT/
WI-7265l	231 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265k	121 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265j	174 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTT/ATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265i	227 T C ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTA TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265h	80 T A ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265g	170 T G ---			AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT

WI-7265f	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265e	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265d	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265c	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265b	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265a	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7281b	183 C ---	---	GATCACCCAGCCACAAAGCCCTTGGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGAGGCCGCGCAG GTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCTGCAAGAGGCCCTCCTC
WI-7281	171 C A ---	---	GATCACCCAGCCACAAAGCCCTTGGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGAGGCCGCGCAG CAGGTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCTGCAAGAGGCCCT

WI-7282b	159	G C ---			TGTCACCTGGCACATTCAATTTCTCAGTTGAAGAAAGAGAAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCACCTCAAAATATGTCAACTNNNNNNNNNT AGGCCCTTTTCATAAAACCAAACT[G/C]TAGCAAGATGCAATGCATGCAAACTCTGTGGTCTCCA GTTGGTTATCTGAATAGTGCACCAATTCACCAAGACAGTCTGAGATTGG
WI-7292	92	T C ---			CTTGATTACTCCACTGAGTGGGAGCATCTCCAGTCTCCCAATTATATCTCCCCCACTCCACTAC TCTCTCCTCCACTTCATTTTCQ[T/C]TTGTCCTTCTCTCTAATCAGTGTTCAGGCTGACTTG GGACAACGATTAATTGATATATTGTCTGTTTCTCTCCCAATAGAAGAAATAGTCATGGAGCC TGAAGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCA ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG CGGT[A/G]TAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T ---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGTGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205	A C ---	---	---	A A C T A T G G C A G T G G T C T G G T T A T A G T A G T A G A G G G G T A T G G T G G T G G C A C C A G G A T A T G G A A A C C A A G G T G G T G G A T A T G G T G G C G G T G T T G A G G A T A T G A T G T T A C A A T G A A G G A G G A A T T T T G A C G G T A G T A A C T A T G G T G G T G G G A A C T A T A A T G A T T T G G A A A T A C A G T G G A C A A C A G C A A T C A A A T T A C T G G A C A C A T G A A A G G G G C A G T T T G G T G G A A A G C T C G G G C A G
WI-7314c	49	G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C T G G G T T T A A T T G G G A G G T C A G A T T G T T C T A C C T C A C T G A G A G G A A C A G A A G G A T A T T G C T C C T T T G C A G C A G T G T A A T A A G T C A A T T A A A A A C T T C C C A G G A T T T C T T G G A C C C A G G A A C A G C C A T G T G G T C C T T C T G T G C A C T A T G A A C G C T T C T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T A T T A A C A A A A C T T G T T T T
WI-7314b	49	G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C T G G G T T T A A T T G G G A G G T C A G A T T G T T C T A C C T C A C T G A G A G G A A C A G A A G G A T A T T G C T C C T T T T G C A G C A G T G T A A T A A G T C A A T T A A A A A C T T C C C A G G A T T T C T T G G A C C C A G G A A C A G C C A T G T G G T C C T T C T G T G C A C T A T G A A C G C T T C T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T T A T T A A C A A A A C T T G T T T T
WI-7314	36	A G ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C T G G G T T T A A G T T G G A G G T C A G T T G T T C T A C C T C A C T G A G A G G A A C A G A A G G A T A T T G C T C C T T T T G C A G C A G T G T A A T A A G T C A A T T A A A A A C T T C C C A G G A T T T C T T G G A C C C A G G A A C A G C C A T G T G G T C C T T C T G T G C A C T A T G A A C G C T T C T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T T A T T A A C A A A A C T T G T T T T
WI-7321b	199	C T ---	---	---	A C T C A G G A A G G G A T G C C C C A T T A A A G T G A C A A A A G G T G G G T G T G G G C A C C A T G G C A T G A G G A A G A A A C A A G G T C C C T G A G C A G G C A C A A G T C C T G A C A G T C A A G G A C T G C T T T G G C A T C C A G G C C T C C A G T C A C C T C A C T G C C A T A C A T T A G A A A T G A G A C A A T C A A A G N N N N N N N A G G T G G C A C A C C C A T C C T T G T T G C T G G G T G T G G C A G C C A C A T C C A A G A C T G G A G C A G C A G G C T G G C C A
WI-7321	199	C T ---	---	---	A G A C A T T C T C G C T T C C C T G A A G A C T G A A G A A G T A G T A G C A T G G G A C C C A C G A A A C T G C C C T G G C T C C A G T G A A A C T T G G G C A C A T G C T A G G T C C A G A A G T C C T A T G T T A A G C C C T G G C A G G C A G G T G T T A T T A A A A T C T G A A T T T G G G A T T T C A A A A G A T A T A T T T A C A T A C A C T G T A T G T T A T A G A A C T T C A T G G A T C A G A T C T G G G C A G C A A C C T A T A A A T C A A C A
WI-7336b	248	A C ---	---	---	C T C T T T C T C A G C A C A T T G A T G G G C A A C T A G A A T T A C A G C A G T T C A A A C T C T A C C A T G G A T A A T G C A A A C A A C C G A A G C T A C A T G C C A A T G A T A G G T G C A A A G A A T A T T G G C A A A G G T G C T T T A C C C T T G A G C C A T T A T T G T C A G A G A A C A A A A G A A C A G A A T C A A T A T A A A T C A A A G A C T A T C T G C A G C T A G T G T G T T C T T T A C A C A C A G T A T A C A C A C A G A C A T C A G A A A A T T C T G T T
WI-7338c	221	A G ---	---	---	

WI-7338b	125	A C	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAATATTGGCAAAAGGTGCTTTTJVCJCCCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATAAAATTCAAAGACTATCTGCAG CTAGTGTTTCTCTTTACACACATATACACAGACATCAGAAAATTCGTGT
WI-7338	125	A C	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAATATTGGCAAAAGGTGCTTTTJVCJCCCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATAAAATTCAAAGACTATCTGCAG CTAGTGTTTCTCTTTACACACATATACACAGACATCAGAAAATTCGTGT
WI-7338	221	A G	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAAGAATATTGGCAAAAGGTGCTTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATAAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACACAGGATATACACAGACATCAGAAAATTCGTGT
WI-7384c	146	T A	---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAAATACCATTAAATACATTTGATTTTCAATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATTTTJAJAAAAATCTTAAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146	T A	---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAAATACCATTAAATACATTTGATTTTCAATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATTTTJAJAAAAATCTTAAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145	T A	---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAAATACCATTAAATACATTTGATTTTCAATTTGATTTGTAACAGGATTTCTTCA CAGATCTCATTTTJAJAAAAATCTTAAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7388c	106	A T	---	---	TGAAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCCCTCCACACTTTT TGAGATCCATCCTTTTATCAAGAAGTCTGAAGCGACTTJAJAAAGGTTTTTGAATTCAGATTTAAAA ACCACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTGTCTCCAAGAACCTTTCCCCCAAGATGTGTATAGTTATGG
WI-7388b	106	A T	---	---	TGAAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCCCTCCACACTTTT TGAGATCCATCCTTTTATCAAGAAGTCTGAAGCGACTTJAJAAAGGTTTTTGAATTCAGATTTAAAA ACCACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTGTCTCCAAGAACCTTTCCCCCAAGATGTGTATAGTTATGG

WI-7388	94	T A	---			TGAAATCCTGGGCTCTTGGCCTGCTCTGTAGCTGGTTATTTTACITTTGCCCCCTCCCCACITTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTCTGTCCAAAGAACTTTTCCCCAAAGATGIGTATAGTTATTGG
WI-7438	64	A G	---			TTAGATTTAATTGGCAACCAGCAACTCACTGCCACCATTCCTGAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACCTGTAAACATAGTTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTCCACTGACTTTTACCA
WI-7454b	152	T C	---			CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C	---			CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C	---			AATTTGAAAATCTGAAAAAAGTGCAATAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACCTCAT GAAAGAAAGCCCTACAATAGGCCCCAGGAGAGCAACGTTTACCAACAATTAT
WI-7464b	168	C A	---			AATTTGAAAATCTGAAAAAAGTGCAATAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACCTCAT GAAAGAAAGCCCTACAATAGGCCCCAGGAGAGCAACGTTTACCAACAATTAT
WI-7464a	103	C A	---			AATTTGAAAATCTGAAAAAAGTGCAATAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTAT GTACAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACCTCAT GAAAGAAAGCCCTACAATAGGCCCCAGGAGAGCAACGTTTACCAACAATTAT
WI-7499b	134	T G	---			CAATTTCTCAATCCAACTAGTCTGTGTCCTAAACCATTCAGACAACTTCCACTTCGAAGGTTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCAIT /GJTAGTCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTTTTTAGGA ACTCTGTACAAAATTCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33	A	G	---	---	CAATTCTCAATCCAACCTAGTCTGNTGCCTAA/GJCCATTCCAGACAAACITTCACACTTCAAGGTTTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCGAGGACATCACGTTCTTTTGAATGCTTCATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTTAGGAACTCTGTACAAAATCCCTTTGAAAATATAAAATTTTGGAAATGAGTGATGA
WI-7506b	118	A	C	---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAATGCATCCAGCAGCAGACCACTTNAAGAGTAGTCTCGTGTGATTCCTAGC/A/CJGGAGAGTTGAGTGCCACAGGTAAGAAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCAGAAGAAAATATTTTAAAATATTGGACCACCTCTGTTCTACCATCCCTACCCACT
WI-7506	118	A	C	---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAATGCATCCAGCAGCAGACCACTTNAAGAGTAGTCTCGTGTGATTCCTAGC/A/CJGGAGAGTTGAGTGCCACAGGTAAGAAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCAGAAGAAAATATTTTAAAATATTGGACCACCTCTGTTCTACCATCCCTACCCACT
WI-7534b	143	C	T	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTCGCAGTGTCAACCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACATATCCCGGTGATAGAAATGCTAAATTGTC/TGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAAAATTTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7534	135	T	C	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGGTTCTTGATGTTCGCAGTGTCAACCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACATATCCCGGTGATAGAAATGCT/CJAAATGTGTCGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTAAAAATTTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7543b	162	G	A	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACAGTCTCTGAGGGAAGCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCCTCTTCTGCTT/GA/JGGAAGACCAGCTTTCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCCCTCTGGCTCTTGGATGTAGTCAGTTA
WI-7543	162	G	A	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACAGTCTCTGAGGGAAGCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCCTCTTCTGCTT/GA/JGGAAGACCAGCTTTCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCCCTCTGGCTCTTGGATGTAGTCAGTTA
WI-7555c	60	T	C	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGT/CJCTATAAGAAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCAATCTCTGTTAAAGCCACTTGGGTCATAAGAAGGGGAAGTAAAAAATGAAGTCTGACTAGAAAATTCATTGACAGAGGCCAAGTACATTTAGTAGTGGCATTTGATATAGTTTTTCAATTTGATGTGCAATTTTGAATTTGAG

[illegible]

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACGATGATGCTTGTAAAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTTCAGACACTTTTGAAGTTTGTGT TCTGTTTGTAAACCTGGCATCTGACACAAAAA[A/T]GTGAAGGCCCTTATCTACATTTCCACCTAC TTTGTAGTGAGAGACAAAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTAQAC[G/A]TAGGAAGAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCG[A/T]CTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA AAATATGCAT/CJCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA TAATAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC/GJATAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGJATCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 C G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	114 C A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7576b	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGCTTGTAAAGAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAGCGGCTAGTTTCAGACACTTTGGAAGTTTGTG TCTGTTTGTTAAACCTGGCATCTGACACAAAAA[A/T]GTTGAAGCCCTTATTCTACATTTCCACCTAC TTTGTAAGTGAGAGAGACAAGAAGCAANNNNNNNNNAAGAAAAATAAAC
WI-7577g	77	T C ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCA[T/C]CAAAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	G C ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA TAAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157	G A ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC[G/A]TAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48	A G ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA TAAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	G A ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T C ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	C A ---	---	AACCATGTTCCCTTCTTTAGCACCAAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCAT/GJCAAAATCGTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTACAC/GJTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATC/GJATCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTTAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTA/GJACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTCCITTA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTGTAGTGA/GIACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTCCITTA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAG[GIA]GTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATTA/GIACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTCTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCT[G]TCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGAAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGGCCAAATGGGTATCC[C]GCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCT[G]TCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGAGTGGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTTGGC[G]GTTAAACCCACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCAAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAG[C]TACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGCAAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7626	144 T C ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGCAAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	---	TCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGTTGTTCTCTAAAJA /GTTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTTATTAGAATTCATATGAC

WI-7689b	134	A G	---	---	---	TCCATAACCGCTGATTCACGGGTCTCTGCTGCGGCCACCCAGATGGGGGAAGACACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGAGCCACCCAGCAAAAGTTGTTCTCTAAAJA /GJTAAGGCAGAGTCACTGGGCAGCTGATACAAATTCGAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7689	121	G A	---	---	---	TCCATAACCGCTGATTCACGGGTCTCTGCTGCGGCCACCCAGATGGGGGAAGACACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGAGCCACCCAGCAAAAJGJTTGTTCTCTAA AATAAGGCAGAGTCACTGGGCAGCTGATACAAATTCGAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G A	---	---	---	TGGAGAACATTCAATTCGCCGTCACTATTCATCAATGAAGATTG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCAACGATGGTAGTGGCAAGAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGGATGTTCCAGTGGATGGGCCACACAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164	T C	---	---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTTACATTTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAAJ/CJGGTCTCTCACTGTTTTTATTTAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C	---	---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTTACATTTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATG/CJAGTAAATGGTCTCACTGTTTTTATTTAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C A	---	---	---	TAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGCCAAAG GTTTCAGAGACTCAGGCCCCAGCACTAAAGCAGTGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCCAACG
WI-7743d	275	C T	---	---	---	TAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGCCAAAG GTTTCAGAGACTCAGGCCCCAGCACTAAAGCAGTGAGC/CJAJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCTCTCAGGCC
WI-7743e	106	C A	---	---	---	TAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGCCAAAG GTTTCAGAGACTCAGGCCCCAGCACTAAAGCAGTGAGC/CJAJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCTCTCAGGCC

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAACTTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATCjA/GjTAGTTAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAAA GATAAATGTGTAATTTTGTATTATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCCACTGCTTTGAACCTGCCTCCCTTCATGCATGGAATTCCTCTCATCTGGAACCATCAGAAACCCCTCACACTGGACTTGCAAAAAGGGTCAAGTATGG[G/C]TTAGGGAACATCCATCCTTGAAGTCAAAAATCTCAATCTTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTTGATAAAAGATTTTCCTATCTTGTTCTGTCAGAGAACCTAATAAGTCTACTTTGCCATTAAAGCGACTAGGGTTCATGCTTTTACCCCTTNNNNNNNNNTTGTAAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAATCAGATCCCAGCTTCGGCATTGTATCAGACCAACAGTGTCTTTCCCGGGGAGGAAACACTTTTAAATACCCCTTTGCAGGCACCACCTTTAATCTGTTT[C/J]ATACCTTGCCTTATAAATGAGCGACTTAAATGATTGAAAATAATGCTGTCTCTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAAATACGTAAATGCATTGGAATAAACTGTCTCCCATTTGCTCTATGAAACTGCACTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCATCATTTACCAATAATTTATTGTCCATTGATGATTTATTATTGTAATGTATCTTGGTCTGC
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAAATACGTAAATGCATTGGAATAAACTGTCTCCCATTTGCTCTATGAAACTGCACTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCATCATTTACCAATAATTTATTGTCCATTGATGATTTATTATTGTAATGTATCTTGGTCTGC
WI-7785	156	T ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAAATACGTAAATGCATTGGAATAAACTGTCTCCCATTTGCTCTATGAAACTGCACTTGGTCATTGTGAATANNI- /TJNNNNNNNGCCAAAGGCTAATCCAAATTATTATCATCATTTACCAATAATTTATTTGTCCATTGATGATTTATTATTGTAATGTATCTTGGTCTGC
WI-7789c	84	G A ---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCAACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCCTGGTGACTCGGGGCTGCTCAGACGACTAGCCCAAGACCATCT
WI-7789b	84	G A ---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCAACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCCTGGTGACTCGGGGCTGCTCAGACGACTAGCCCAAGACCATCT

WI-7789	73 GA ---	---	TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGATTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAAGTGGGGCTGTCTCAGACGACTAGCCACAGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACTCTTCAAACCTTACAGTCTTCCCTAAGGTACTCTTCATGAGATTCAATCCATT TACTAATGCTGATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAAGTCTC/TJTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7790	190 CT ---	---	AATTGTCAGTCACTCTTCAAACCTTACAGTCTTCCCTAAGGTACTCTTCATGAGATTCAATCCATT TACTAATGCTGATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAAGTCTC/TJTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAATTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAATTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATCTG
WI-7814c	41 GA ---	---	TTCTCTCATTTTATCCCTCACTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCATTTTATCCCTCACTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCATTTTATCCCTCACTGTAG[G/A]CATGCCAGTCCCGTTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/][T]TAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7830c	54	GA	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7830b	134	GA	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAAC[G/A]ATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7830	44	A G	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C/][T]AAATGAGCGAGGCAATTTCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAAATGAGCGAGGCAATTTCTAGTCTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/][T]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C/][T]AAATGAGCGAGGCAATTTCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAAATGAGCGAGGCAATTTCTAGTCTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/][T]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T	---	---	CCACTTCCTATCTGATTTTCCAGC/TTAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTCAAGGTGCTTCCAACCTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T	---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTTCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTCAAGGTGCTTCCAACCTGAAATCTCAATGTTCTCAGTA/C/TTGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C	---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTACTAGTCCCC CTAACAATTACCCTGTCAAGAGG/C/GAGTGCAGCTCAGGTGGATTAAATGTGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAGTAACCAATTTCTGTTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTTGGATTAAAGG
WI-7867b	92 A C	---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTACTAGTCCCC CTAACAATTACCCTGTCAAGAGG/C/GAGTGCAGCTCAGGTGGATTAAATGTGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAGTAACCAATTTCTGTTCTTGTCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTTGGATTAAAGG
WI-7868c	173 C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACCTGCTCCCTCTGATCCTCCATCAGGCGCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGTCTTACCCCTATTCAAGCA/C/TTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868b	173 C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /C/TCACCCCAACCTGCTCCCTCTGATCCTCCATCAGGCGCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTCCCTGTCTTACCCCTATTCAAGCAACTAGAGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868	66 T C	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGGGGAATCC/C/ATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGA GCTGCAATGCCTGCAAAAATGAAATCCAATGAGCACTAGATATTAAAAACATCAATTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATAATCAATTG
WI-7870b	85 T C	---	---	

WI-7870	76 C T	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCAGCTATTAATACCTCTGCAGTGATTAGAAAGG GTGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAAATGAAATATAATGTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTAATGCCATC TTTATCATGAAGCAGACATCAATTACAAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C	---	---	TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGGCGGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGAGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTTCTCCAGAGACACAAGAAAG
WI-7889b	54 C	---	---	TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGGCGGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGAGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTTCTCCAGAGACACAAGAAAG
WI-7894c	142 A G	---	---	AGCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAATAATTTGCATTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G	---	---	AGCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAATAATTTGCATTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACCTCAACTATAGAGACATTAAAGAAATC

WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T ---			AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCCTTTTAAACAACTCCAGGCCCTGGTGGGGTGGTGGGTTATGGGGCAGCGCCGCGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCTATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T ---			AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCCTTTTAAACAACTCCAGGCCCTGGTGGGGTGGTGGGTTATGGGGCAGCGCCGCGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCTATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T	---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTTATAAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGGTGGTCGT CACTCAGTCGCTCGCATGCTCTCTGTCTACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCT TTTTAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGGTGGTCGTAC TCAGTCGCTCGCATGCTCTCTGTCTACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150 C A	---	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCA TACAATGCAATACCTT[C/A]ATTTTAATACTCTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC ACTTTGGAGATCAGAAAATTTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTT ATTTACAATGCAATACCTTACATTTTAATACTCTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A	---	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCA TACAATGCAATACCTT[C/A]ATTTTAATACTCTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	---	AAGAGCCAGCAGGTCAAAAGGCCAACACAAACCATTAAGCAGCCACACAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCCGAGTCTGCCACCTG
WI-7947	203 G T	---	---	---	AAGAGCCAGCAGGTCAAAAGGCCAACACAAACCATTAAGCAGCCACACAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCCGAGTCTGCCACCTG
WI-7963b	145 T C	---	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAAGTAAGACTAATTTATTTAAAAATAAAATGCC ACAAATTTCAATTTCTCCTCTAAGTATTACAATGGAGTTTATCTCTGCCCTAAAAAGTGGAGAAAT TGAGTGAATGA[T/C]AATTTTGTAATTTAGGATAAGATCCAAGTATTTTCCCAACTCTTGTGTTCCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTCAITTAAGGCGAGAAGACGCGAAAA

[illegible]

WI-8021b	57	C T ---			ACAACTCAGAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAC[CT]GATCCC ACGTCTTAGAACCTTCAACACAGGAGTTTCTTGAGTAGTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCTTTCACCTTGAGATCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGTGATTCGAATTCGGTGAATGGCA
WI-8021	57	C T ---			ACAACTCAGAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAAC[CT]GATCCC ACGTCTTAGAACCTTCAACACAGGAGTTTCTTGAGTAGTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCTTTCACCTTGAGATCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGTGATTCGAATTCGGTGAATGGCA
WI-8024c	206	A G ---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGCGAGAGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCACCACCAACACCATTTACGCCGCTTAGCCTCTAA TTCC[AG]CTCTAGAACAGCTGGCCCTGGTGTGCTAGTACACAAAGGAAGAGC
WI-8024b	206	A G ---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGCGAGAGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCACCACCAACACCATTTACGCCGCTTAGCCTCTAA TTCC[AG]CTCTAGAACAGCTGGCCCTGGTGTGCTAGTACACAAAGGAAGAGC
WI-8077	167	A G ---			GAATGAGCCTTCTAGCGCCGAGGGACCTGCTGCTGTTTGGCCTGCACATGCATCTATGGAATGC TTTTTGCCCAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAAAC[AG]TAAATCTCATCAGATGGATTTTATTAAACGTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G C ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GC]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---	---	TCTAGTTTAATCAAAGCAATTGCANTTTGGATTTTGGAAATGA[C]TCACTCCCTTCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGATAGCTGTTGTTTCTTAGCCTTGAAGA TGACAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---	---	TCTAGGTTTAATCAAAGCAATTGCANTTTGGATTTTGGAAATGACCACCTCCCTTCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC[C]TGGCAATACAGAATGATAGCTGTTGTTTCTTAGCCTTGAAGA TGACAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAAATGGCAGCGGCTCGGGAAG AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8171c	46 A G ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAA[C]GTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC
WI-8171a	46 A G ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAA[C]GTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC
WI-8171b	298 T C ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAAATGGCAGCAGGCGCTCGGGAAG AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8314b	85 G C ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATTAGGGGTAAACCACT
WI-8314	78 C/G ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATTAGGGGTAAACCACT

WI-8321	178	G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTCAAGAGCTGCTGTTACTAGTCTCTGAGAAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAAGATG/AJAGTATCTTAGTATCTTCTTA TTTGGCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTCAAGAGCTGCTGTTACTAGTCTCTGAGAAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAAGATG/AJAGTATCTTAGTATCTTCTTA TTTGGCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCG/AJCGCTTAGAAACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCAGCAATGCCTACTGCACTACTAGTAAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGATGATTAAGTGTGATGCACA
WI-8332	114	A C ---	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCG/AJCGCTTAGAAACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCAGCAATGCCTACTGCACTACTAGTAAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGATGATTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCAACAGGCCCTCCTCCAAACACGTGGGG
WI-8378	308	T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCAACAGGCCCTCCTCCAAACACGTGGGG
WI-8426	184	T G ---	---	---	TTTAGCACATATTAGCATTAAAGCCTCAAAGATACAGCAATATGTTACATTCTCTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAAATGTAACTCCGACTGTGCCTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTCTGTGGGNGGGTGGCTTTGCTTGAACCTCCATTCTGT/GGCCCTGTAGCTGGTG AGGCTGGGAGTATGGANGNCGGGGCGCTTGGONATNGNATTCAGTGAG
WI-8450h	61	C A ---	---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTC/AJCA TCTTCTCTATCTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTTAAGA AAAAACCTCCCAAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTAT

WI-8450g	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACAT/CJACACTCCAT CTTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450f	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTAT/CJTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450e	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTAT/CJTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450d	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450c	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTAT/CJACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450b	61 C A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACT/CJAJCA TCTTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8450a	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACAT/CJACACTCCAT CTTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAI
WI-8458b	60 A G ---				CAAGGAAAGCTGCAGTCTCATAACTTCAAGAGTTACAAAAATACGTATTTTAAJAGJCTA CAATTCAGATTAGCATCCAAACCTACAAACATGATGATACATTGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTACTTGTGAAAACTTTATTGTGCACAGT GACATCCATCCGCCAGACTTAATGTTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105	A T ---	---	CTTCTCTCCAAAATCTACATGAATACTTTGAAGACAATATAACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAAATCATTTT[A/J]NNNNNNNNCCCTTGCTCTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461b	38	T C ---	---	CTTCTCTCCAAAATCTACATGAATACTTTGAAGACAAT[TC/J]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATAATCATTTTNNNNNNNNCCCTTGCTCTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	38	T C ---	---	CTTCTCTCCAAAATCTACATGAATACTTTGAAGACAATATAACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAATCATTTT[A/J]NNNNNNNNCCCTTGCTCTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	105	A T ---	---	CTTCTCTCCAAAATCTACATGAATACTTTGAAGACAATATAACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAATCATTTT[A/J]NNNNNNNNCCCTTGCTCTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-9438	77	A G ---	---	ATCAGAAAAACATGATCGGGAGAGAAATTATTA ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATCCAGTCTGTAGCTCAGTACCTGT[TC/J]TGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAAG
WI-9439b	101	C T ---	---	ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[TC/J]CCAGTCTGTAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAAG
WI-9439a	76	C T ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[TC/J]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTNCCCCTACTNTTATCACTGTGCTCTGCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9446b	75	T C ---	---	

WI-9446	75 T C ---	---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTATAAAAAAT/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAAAAGCCTTTTAAATTA
				TACTCATCTTCATATGTGTGTTGTNCCCTACTNNTATCACTGTGCTCTCTGTCTTTTGCTACCTATGNGAACTGCACACTATCTGTGGCAATATGT
WI-9497b	185 A ---	---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTTGAGATAATTATTCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGATATCTAGACATATATCTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAGTATGTTAATGTCACTTGGAACTTCTACATGGAAAAGCCAAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTTGAGATAATTATTCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGATATCTAGACATATATCTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAGTATGTTAATGTCACTTGGAACTTCTACATGGAAAAGCCAAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	---	GTGAAAAAGTTTTCTATTCTCATTCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTGCAGCATTCAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACAGACTCAGACAAATTACAAACTATTTCCAGCATGATCTATGGTGATTTCCACACATTTGTA/C]A]AGTGAAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	---	GTGAAAAAGTTTTCTATTCTATTCATCATACAATAGATTGTGCTAAG[G/A]ATCATTTTGGAAAGATGTGCAGCATTCAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACAGACTCAGACAAATTACAAACTATTTCCAGCATGATCTATGGTGATTTCCACACATTTGTACAGTGAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	---	AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGACAAGCATCAGTGATGATCTACTGCCTTNNCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATGCAATACACCCAAAGAACACTAGAGTCTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTGGT/C]GCTGGATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	---	CCAAAAAGCCAAACCATTCATATGTATGGATTTCATAAAACATTTATTGATCCTTTTTTGAGGTAAGTATAAATACCTTTACATGGCTAACCTTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGACTCTTTAATCAAGTTAAATAATCTGCTTTAGAAGGCGACAAATGATCATACTTCAGATTAAAAATACAGGTAAGTATTCAGGGNTAAAAATGGTACAAAAAAGGCTGTAACTCTTTTNNCTTCACATTGATCACA
WI-9625b	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTTAAACAAATAGCTACCATATATTGTATCTNCTCTTGGGAAAAAACTTTGGAAAAAAACACGCACATAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTA/TGTTTACCAATTTTATATTGACATAAAGTAGCAGACTAGTTATTTTCATTTAAAAAAACACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAACAATAGCTACCATATATTGTATCTNCTCCTTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAACTAGGGTTGTGGACAAGTTACTTCTATGTGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTAATAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATGCTAGACCTAAAAATCCAAAGCT TACAACTCTGTGTCCTTACCTGATACATTTATCCATTTACTTTCATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTTCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	---	GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC[C/A]ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAATAACTTGAAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCG[G/T]CATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT[C]CCCTCTGTGCGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACATCATGTACACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGATAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCCCTGGAGCGGGGGTGTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTATGTTGGTGGCCACATGTCGTGATTGCTGTC
WI-9738	40	C A ---	---	TGGACCAACACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACATCATGTACACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGATAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCCCTGGAGCGGGGGTGTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTATGTTGGTGGCCACATGTCGTGATTGCTGTC
WI-9756	47	A ---	---	ACTGAAATGTAAATGGCCAAAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACATCAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCACATTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTCCACAACACACAGATATACACATTTTGGGAG ATTCCACTTAACCACCTTGATTCTTCACITTTTTTAIGATTTAAACICTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAGAAGAATCTTGTTCGCAAGGTCAATTTTATACATTTA A[A/G]TAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTAAATCCAGGCGGGGAAAATGGATACITTTTCATATGCTCTGTACCCAACTATAAATTTTG GTTCTCATGCACCATTTTCATTTTGCCTTCTCACTCCAAAGTACCAGTATTTTACCAATTTG[A/C]CTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTTATTACACACTTTGCCTCA AAGAAATGTCAGTCAGGACTAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTGCCTCCTCATGCCACTCCCTCAGCCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGGCTGACAAATGCAGTTTC[C/A]TGGATCCCACCCAGGA CTCAAAAACCTAGGAATTGGGAGAAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAATGGACTAAAGTTTGAAGACCAGACATGGAAGGTTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATATATTATTAACACTT AGGATTATACACACAATAAACCGTCTGTAAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAAGAGGGGGATGTTACTTGATATGCTGTG
WI-9880c	222	G A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTCTCTGTGTGGGTTGAGTTTTTATGATACTCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTTGGACTATATAAGATCCCTCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157 C A ---	---	GAAC TAAC ACC TTT CTG CAT GGA TTT TCT GAT TTT TCG CAG TTA CCA ATA AAT G TTT ATT AG ATC ACT GGT GCT TCT G TGT GGG GTT GAG TTT TTT ATG ATA TCT CCT GTT AG ACC CAT AAG G GAG GCT GTGA GTT G TTT TCT ACAT CCT TGG A[C/A]TATAA GAT CCT CTT TTA AAT ATATA TTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108 C T ---	---	GAAC TAAC ACC TTT CTG CAT GGA TTT TCT GAT TTT TCG CAG TTA CCA ATA AAT G TTT ATT AG ATC ACT GGT GCT TCT G TGT GGG GTT GAG TTT TTT ATG ATA TCT CCT GTT AG ACC CAT AAG G GAG GCTGT TGAGT GTT TCT ACAT CCT TGG ACT ATATAAGAT CCT CTT TTA AAT ATATA TTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127 C T ---	---	ACAC TGCAGG CACTCCAATCTNACAGACATATGCAC TCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTAAAAACAACGCC CAGTTATCAGAGTTCTN TTTTGT[C/T]CACC ATTTCCATAACAAAAGAGCTACACAAAATTN GGGGGAGANACTCTCTTTGGAGACTGCACACATT TGCAGAGGGGTGCATGAATAATGATTCCAAA
FB25G10b	109 A G ---	---	TCCCTCAATGACAGATGAAC TAAATTTCTCTTGGGTAGAAATAC TTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA[A/G]TGATTTTATAGATCCTCCCCCAG TGACAAAGTAACTGAAC TGAAC TGAAC TATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109 A G ---	---	TCCCTCAATGACAGATGAAC TAAATTTCTCTTGGGTAGAAATAC TTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA[A/G]TGATTTTATAGATCCTCCCCCAG TGACAAAGTAACTGAAC TGAAC TATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102 C A ---	---	ACAA CGCTGAAC TCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACACAATTTA GATGAAC TGAATTAAGNTAAATAAATAAATAAAT[C/A]CAATTT CAGNAACAAAATCAAAC ATTAAGGNTCCCTGNNATATTTCTTAAACCCTAATGAGATTTCACTGNNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCTATTAAACC CAGTCTAGGGATTCTG
NIB551	161 C T ---	---	CGTCTTTCTCTTTT GAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTTGTCCC TACTGAGCTTGGGCCAGGTGTACTTAGGAACCCAATCCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51 G T ---	---	AGCATAGAAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTCCCTTT[G/T]AATTTGTGAGTTT ATTCTGGAAAATCTTTT GAGTTAAAATAAGGATCTTAGAGACGACCTCGAAGTACAGGCCCTAAA GAGAAATTGCCCTCAAAACCACAAGTCTGTAAC TCTCCCTTTCTGTCAATTTGGTTGTCTTTAAATA TTGCAAAAGTCTTGATGCTAAACAGTATTTGGAGTGTCTTTTCAAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATCCCTTGTTAAAGACTGAATTTGTAAACG CATTCAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGACGTTJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTACAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTGGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACAGGAAGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGAAC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAACAGTTTCCTTTAATTGTAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACACGCCCTCTTT
ESTC122	34	---	---	---	GACAAATAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTAIGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30						GGTAAAGTCTAAATTACTGCCTTAGCAAAACNCATGTTGTCAAGTTTTCCTGCTGCA
ESTC137	21						CCAGTTGGCTCTGICCTCANAGTCTCTCTCCATGIGGCAACA
ESTC139	45						AGGAGCACAGCCTAAGGACATGAAGTCAGAGTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20						CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCCTGGTG
ESTC142	72						CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCAATTCATTCTCTAACAAACA
ESTC143	29						GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26						AAATCCATATTTTCTTGACATGAGGNGCTTTTTAGCAGCATTTCCG
ESTC146	20						CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42						TCCTTGGTGTCTACACAGACACTTAAGTACTGTATCGCTGTATGACGGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGTCTCTGAG
ESTC149	28						TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28						GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20						CCAGGAAACAAGCAGCACACANACTTATAGAATACTTTGGTTTAAAAATTTATCATAATCAATATT AACTCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49						GAAGCTAAGGCCCATTTTCTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37						TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTTACA
ESTC156	32						GCAGCATTTGTGACAGGAGAGCGCAACAAANCCCTGGCTGCCCTGGGATGGAGCGGGGGGCGCTCA CCACCACCTGCAT
ESTC158	35						ACCAAGCCCTGGGATTTACTGTCTTGTGATGACTACANGGCTTTGCACAGCTGAGATGCTTCAGTGTGC AA
ESTC159	31						AGCTGGCAAGAGACTTCTGAGGCACATCAGNTAGTGGTGGTCAATTTAGGCACGGTCTGGTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGCATGATCATACCCACAAGGACAGGTT TTCTAGCAATTGCTGGTGAGTGGGGCCCTGAGCTGGGNGCAGTCGGCAGTGTCACTGGGCCCGTTTG GGACTGGGTGA
ESTC160	38	---	---	---	CTCTCGTCGGTTTGCAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG TCATTCTCCATAGAATAATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC162	36	---	---	---	GTCTCTGGTGTGCAGGAATCANITTTGCTGGATTAGAGGAAGGTGCCCGCTGTGTTCATGACTT
ESTC164	31	---	---	---	CACCTCCTCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCCTTTATTTCTATTAATAACCTTTTAT TCTCTTTATCCCATAAAAAGGCAACCAA
ESTC169	22	---	---	---	TCAGACACTGCGGACATCAGCATTGTCTCNITGTACAGCTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC176	23	---	---	---	TAGGGATTCCAAAGTTGCCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC177	42	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGTAAATGTCTCAGCTTG ATTTTCACCTCA
ESTC18	29	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCCNTGTCAACCTCAAAACAGATGATCACTCACTGTGCTTCCAT CTTGC
ESTC181	21	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA TCCTCAAATACCACCTTTCCCTAACTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAAATGGGTTAC CTTTCAGGGG
ESTC186	43	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCNCGCAAAGTCTCCACAAGCACA AAGATTAGACAGACCGCGTATAGTAAGCTCTGNGGAACTCCAAGATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC187	24	---	---	---	TTTGGTGAAAATCCCAATATATGAGTTTAAAAAATAATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG
ESTC188	25	---	---	---	
ESTC189	27	---	---	---	
ESTC196	42	---	---	---	
ESTC197	26	---	---	---	
ESTC20	33	---	---	---	
ESTC200	44	---	---	---	

ESTC201	35	---	---	---	TCCTACTTGGGTAGTTAGCAAAACATTTTAAAAACCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACGCGNCGCGCTGGGTGGCGGCCCCAGAAAGCGTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	ACACCTAACAGGTTAAATATCCAAAATNAATTTACTGCAACTTTTGTAGAAATTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCTCTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCTCTCTCANACCAGGGGCGAGGAGGAGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAAATTAATTTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATTAACAAGTTTCAT AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCTGTGGGGTGAGCACACAGCAAAAANGGGGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAAAATTATGGGTTTATTCTTATTCTAATTNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAANGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCTCACATATTACAAAAATACACANAACACACACACACACACACACA
ESTC225	20	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGATGATCG
ESTC23	27	---	---	---	TTCTACTTTATTTCATATCCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	GGCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTTAGTCATATTCCTCCANCAACAGCATGATAAAAATAATTTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNNTTCTCCTCTATTCTCTATAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCGCGCCCTCAATTCATATTTATTCTTGAGCCGCTTGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATATNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTCCTCAGA
ESTC33	25	---	---	---	AGCACTTCAGCTCCTTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGCTTNGGTCACAGAACTCAGACCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTATGCTGATGGAAGAAACCAT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAATAATTTTGACTTGTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCTCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCGCTGCCATGGCCAGGAGCAGCTGGTCCGGANCCGGGCAGATG TTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGCCCTCCAGTCCNCTCTGGGCACAGATCCACCAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGCGTGTCTCATCTGTGAAATTCACAGGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTCGCTAA
ESTC7	45	---	---	---	AGTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCAGCATGGAGATTTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGCTTTGGCGTGACGCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAATTCACAGCTACAGGAAATCTAGAACAAAATCAAAATATTCATCACNTTGGGTTGAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTCTGTCCCATCGGAACACAGAGTTTCCCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGNTCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTAGAC TTTCACAAAACCT
ESTC85	28	---	---	---	TTTAGCTGTATACCAAGTTTCCATAAANCTGTCTGTCTGGTGGGAGGCTACAGCCTGACCACATTG TTTGC
ESTC89	22	---	---	---	ATTGCAAAGGAAGTGGAACGTGNTCAAACAGAAAATGGTGACAAATGA
ESTC90	33	---	---	---	CTGGTCTCTTCGCTTGGCATTCGCTCCTCTCNGGCCAGTGCTCCACCAAGTGCTTCCCCGATGAT
ESTC93	29	---	---	---	CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTACAGGCGAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCCTCTTCCAGAAGTTGNAGACGCTATTAGTTTGATTATCTGTG
DWU-100	127	CT	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTTCTCCA/C/TGCCAG ATCTTATCAATGATCTTTACCTAAGAAACAGCAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGGGATTTTTCACAAAATCAAAGAAGAAAGGCTTAGCTG
DWU-177	77	AG	---	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTTTCAAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC/AG/GCCCTATTACAGTAGCCAAACGATGAAAACACCCCAAGCTATATATTACCA GATGAAGGATAAACAATAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213	AC	---	---	CAAAATCCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCAATCATGCCAGCTTCTGTATATGATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG/ACT/GGGAAACCAAGCCCTATCTGAGTCTTGGCTCCCTCC

EST10398 2a	147	CT	---			TGCTGGGGTGCAAGGCTGCAACAAAGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCACACGGAGAAAG CATTTGTTTCTTCTGCGGCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTGG
ESTD-C7	14	GC	---			ATATCGTGGCCTTA[G/CTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90	TC	---			CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACCTTCTTTT[C/CTCTCTTAGAGTCTACCGG
ESTD- GPPK2L	38	GA	---			AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTTACC[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82	AG	---			CTGGGCTCGOCCGACGAGCTGCTGGCACTGGACGGGGGGGGCCAGGCTCACCTCTATAGTGGGGTCG TATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD- HRASa	37	CT	---			CTGGGCTCGOCCGACGAGCTGCTGGCACTGGACGG[C/T]GGCGCCAGGCTCACTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81	AG	---			GGAGGCAGGAGGTGGGGGGGGTCTGCTGCTCCAGGTCCACAGACCAGAGAGCGGCCTCAGTG TATCCCCACCCCA[A/G]GTGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	AG	---			GTGACCTTCTCAGCTTAA[A/G]AAACTTTACCGGAGAGAAATTAATATATGCTATGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGAGAGGTATGTAACA
EST36751 7	36	CT	---			CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTA AAATTGAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109	AG	---			CACGTGAAAGGAGCTATTTTGGAGGCTTAAAGTAAAGAACTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTAAACAAAT[A/G]TTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGATCCGTACCGTCTGACGTTTTTGAACAATACA GATGCTTCCCTTTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121	CT	---			GGCTCTATACCCCTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT GTGGACAGCACCTGGCTTTCACACACCTACGTCCACTTCCAAGGTAAAGGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31	CT	---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180	AG	---			AAATCCAGCACCTTTAGGAGGCTGAGGCAGGCATATCACAGAGGTCAAGAGTTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCTAGGTGGTGCATGCTGT AAATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGA GATGGCACCATTCACACTCCAGCCTGGGCAACAGAGTAAAACTCTGCTTC

EST70523 3	182 G T ---	---	---	TTCCGCCAGCCCCCATCTTGGCACCTGGTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTCGGTAACTCCGGCGGGCGCTCTTGAGCACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCAGGGGCCAGCCCTG/TCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGAGTGTC/CCACGTG
ESTD- APOA2	101 C T ---	---	---	CCAGGTGTTGTGGCACGTGCCTGTATCCAGCTACTCGGAGACTGAGGCATGAGAACTCTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCG/TCGCCACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATGGTTACAGGAGGCTTT AAGTTACAGCATCTTGGCTCACATGAAGGCCAAATCCGAGAGAC/CTCTAGAAGATACACGAGAC CGAATGTATCAAAATGGACATTACAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6	137 C ---	---	---	AGACATGAAGGAGTTGAAGCCTACAAATCGAACTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGAGCTGACGGCGCCAGGCCCGGTGGCGCGGACATGGAGGA CGTGGCGGGCGCTGTGTCAGTACCGGGCGAGGTGCAGGCCATGCTGGCCAGAGCAACCGGAGGAGC TGGGGTGGGCTCGCTCCACCTGGCAAGCTGGTAAGCGGCTCCTC
EST43211 8	132 C ---	---	---	CGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATCGCGATGACCTGCAGAAAGCGC TGCGAGTGTACAGGCGGGCGCCGAGGGCGCCGAGCGGCTCAGCGCCATCCGCGAGCGCTG GGGCCCTGGTGAACAGGGCGCGTGGCGGGCGCCACTGTGGGCTC
ESTD- ARSB	126 A ---	---	---	GGAAAGAAATGGAGCCTGTGGAAAGGAGGGCTCCGAGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGGCGTGAAGACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGACGTGGGAAACCATCAGTGAA GGAAAGCCCATCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAAC
EST36770 4	144 C ---	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGGCTGGGCTGACCAAAATATACCTGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAGGCCCTAAAGAGGCTTATG
EST26021 1	137 A ---	---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGGTTGAGTGCATGTTGCAAACTGT CCATAAAGTAATTTGTGAAGAGGAGCAAGAGAACATCTCTGCAGCACTTCACTACCAAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29 A G ---	---	---	GGGCAACATAGTGAAACCCCATCTCTACAI/GIAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTCCACTGCA

ESTD- CB22	119 C T ---			GGCAAGTTTTATTAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCTGGATACAAAAG ACAGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCAATTATGGTCTTCCCGGGCTTCTCTCACACAC TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTCCACCCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA ACGAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTACCCCGACCACTGGAGCTGAGCTGGTGGTGAATGG GAAGAGGTGCACAGTGGGGTCAGACAGACCCGACGCCCTCAAGGAG GTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTTCGCGCTC TCTGCTCTCGAACCCAGGCGATGGAGAAATCCACGGACACAGGGCGTGAGGGAGCCAGAGCCACCTG TGCACAGGTAG/CCTACATGCTCTGTCTTGTCAACAGAGTCTTACCAGAGGGGTCTGTCTGCTGCC ACCATCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGGTG TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGGTTCATTTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGAC/CJTATCTTC TGATTTAGGGAAGCAGCATTCCCTTGGACATCTGAAAGTACAGCCCTCTTCTCTCCACCCAAATGCT GCTTCTCTCTTCATCTCTGATGGAAGTCTTCAACACCATTTCCATACC
ESTD- CB23	136 C ---			TTTTCTGTTTACCTGTTCAGATCCCTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTTCTTAAACAATAAATGAAAGTCCAAATTTACTCTTGATCCATCGACTGCAGAAATAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTCAATGCAGTAG CAGGCCAGGTGGTCAGGTGGTCACCATCCCGGACAGAGAACAGGTACGCCACCACTATGCA/GJCA GGTCTCATCAITGAAGCTGCTCTCAGGGTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG AAAAAACATTTTAAACACCTTTTCAATCATATACACCATA/GJATTTCCATTTTACATAAGTCA GTTTGAGCTGAGTTTTCCAAATCTTGAATCTAAAAIGTCATACTGATTAAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATAICTGGATTAAATATGCCCCA TATCTGCATGTC
ESTD- CB24	145 A ---			CATCCCCAAGCCCATCTTAGCCACTGGCAATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCGCCCTACCTTTGTAGTCCATGGAAAGGCTCTCTGCGGCGGTG GGGTGTGTGGCTATGTGTGCTTGTGTAG/CJTGGGGGCTTGTGTTTGTGTTGACTTGTGCTGCTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC
ESTD- CB25	146 A G ---			
ESTD- CB27	125 C T ---			
ESTD- D4S338	59 A T ---			
ESTD- CYP2D6	61 A G ---			
ESTD- D11S1873	40 A C ---			
ESTD- D17S33b	169 C T ---			

ESTD- D17S33a	75 C T ---	---	CATCCCCAGCCCATCCTTAGCCACTGGGCAATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTTAGTCCATGGGAAGGCTCCTCTGGGGCG GTGGGGTGTGGCTATGTGGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATTGGGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTAACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATTCCTTGAACCC[A /G]GAGGCAGAGCTTGCACTGAGCAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGGA GACTCTGCTCAAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAANAATCCAATAAAGTACACTGTATAAAGAATTTAACAGAAATATCATTTGT TTATCAAACATTTATCACITATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTAATGCTGATGTTTGGCTGATGTTCCGAGGAGCCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAAACATACTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCTGTTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAAACATACTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCTGTTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTCTACAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCGAGTCTCTCTCTACATCCTTTTCAAAACATTTTCATCCTGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGCTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTACCTCTGGTGGAGAACCAACTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGMACAGAT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTGGGCTCCAC GTTCCATGGGTGTGGGCTGGGACCTCACTGCTCCCTGGGAGAGGAGGAGTGGGAGGGAGGA CAGAAATGCTGATTATCTGTGGAGAACCAACTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---	---	TCTGCTTTGGTCAGGAGGTGCCCGGCGAGGCCAGGAGCTGGAGATGGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTAGAGCCCCATCCACCCAGCCACCACTGACTCTCCCGGACCCG TCCCACACGGTCTCCAGGACTCCGACAGCCCCCGCCCAACACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	AAGACGATGCCAGGATGAGCGGACAGTAGGAGGCGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCACACAGGTGTAGTTACAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD- ERB2	93 C T ---	---	TCTTCAGGATCCGCATCTCGCCCTGGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTAGGGGGTGGTGGTCACTGC/TGGGGCCGGTGCAGACCCACGCGGCTGGGAGACTTCA CCCCGCTCACTCCGTTCTCGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	43 A G ---	---	ACTCACAGTCTTTTAAGTGAATGTCGAGAAAGAGGCACCA/GJGGAAGCCGCTCCTGGCGCCTG GCAGTCGGTGGGACGGGATGGTCTGGCTGTTGAGATTCTCAAAGGCGGACGATGCTGGACACA CACAGACTATTTTAGATTTCTTTTGGCTTTTGAACCCAGGACGCAATGCAAAAACCTTTTGAG AGGTAGGAGGGTGGGAAGAAACCAACATGTCTTTTCAGAAGTTAGTTG
ESTD-F9	111 A G ---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGTATGATGTTTA/GJGTCAAACCTTCATTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---	---	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGA GAAGCTTGCAGCTCATGACAAATTTGAAGCTGACAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTGAACATTTGAAGTTGTTTGAACCTGGTGTCACTTTAATACAACTAG CAGACGGAACTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---	---	CGCAGACCGGTCAAGTGGGGTCGGGAGTGTGGAGGGAAGGAGGGAACCTGGGGTTAGGGACT TTCCGGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCAACTGGCTAA GTGAAGGGACCTCTGGTCGCACCGTGTGTTCTGTGCCCCCTGTTTCACTGTCTGTCTGCCGAGT/C GJGACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A/G ---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCAACATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCAGCGGGCGCTGAGCCCCAGGGAGCAGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCCAAGAGACCGGGCTC[AT] AGGATCCCAAGGCCCAACTCCCGGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGTCACAAACCAAC[AG]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCTTAGG
ESTD-HT2	154 G ---	---	GGCTAAATTTCCGAGCACTTTGCATAGACTGTTTTATTTGACTTGACAGGATTTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTACATCCCTGGGAGTTAATAGTGCATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACACAGACACACCTT
ESTD-HT5	149 C ---	---	AACACACAAGCCCGAGCAATTTGAATCGCGACCCCTGGTTTACAAGACCAAGTCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTCTTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCTACAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAAGCCCTCTTCTCTCTCCCTTGGG CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCTGAAACCAAGCAAGAGAAAGAG[AG]CCCCAGA AATCACAGGTGGGCACGTCGCTACCGCATCTCCCTTCTACAGGGGAATTTACAGGGTAAAC! ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGGTGC[CT]CTGGGAGAAAGGAAGATG TTCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGCGAGTGGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACCTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTTATTTTITG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGGC[AG]CAATCTCGGCTCACTGCAAGCT CTGCCTCTGGGTTTCATGCCATTCTCTGCTCAGCCTCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGGCTAAATTTTGTATTTTGTAGTAGACGGAGTTCACCGT
ESTD-IL1B	99 A G ---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGTCTCTACCTTGGGTGCTGTTCTCTGCTC[AG]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGTGGCTGGACCCAGGCCAGCTCTGCAGCAGGGAGGAGCTGGCTGGCTCGTGAAGCATG TGGGGGTAGCCAGGGGCCCAAGGAGGGCACTGGCTTTCAGCCTGCTGAGCCTGCTGCTGCTGCTG TJCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGGCCTCTGCTGCTGCTGCTGCTGCTGCTG CTCTGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGC

EST45311 0	151 C T ---	---	---	GGCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACAAACACACAAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TJACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---	---	---	TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTCTGAGGATGTCAACCAATTAACCAGAAAT CCAGTTATTTTCJA/GJCCCTCAAATGACAGCATGGCGCGGGTGCTCTGGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTGCCATGGAGACTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGTGGCTGTTCTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---	---	---	ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCCAACTGTCTCCAGGGCTGCAGATGTCTG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T ---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTGTGTTTAGCATTACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTG/TJAAAGTGCCAGTATCCAGAGTTTTGGTTTTTGAACAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGTGTCATGCA
ESTD- KRT10b	183 C T ---	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACCTATTACTTCTAIA/ GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCAIC/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---	---	---	ACCTCACCCCTCCCTTAGCC/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGCTCAGGTTTACCAIC/TJGTCAACATTGACACA
EST75099 6	82 C T ---	---	---	CACCTGTGTGTGTAGATCTCCTCAGTGGCGGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TJGGGGGCAACCGGAAGACCCTCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTCTCCTTGGCGCTCTTGAGGTGTTG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGTAACCGTAGCAAACTGCATTGGTATTAGA AAAATAAAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAGGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACTGTGATTCTCCCAATCTTGGCTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGACJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCAGGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGACCTCAACCTCCAGCTTCTTCAGCTCTGCCCTGCTCCTGCCTGCA AGGTTTGTCTTAATTCATCAATCAATGTCTCTCATCTTTAGCCTTGGGTTTGTGTTG TTCTCTGTTTTTGTCTTAGTATCTGACTACTTTTAAATAAAAAAGAGATGTATCTAAACAAAAATAG AGATTGTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCTCCCTCCAGCTCTGTCCTAGCCTTGAACCTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCOAAGGGTTTGGTCAAGTTGCTGATTACCCCTTGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCTTACAGATCCACAGACTGATATGGCTGGT AACATGGACTTGATATTTGTACAAAAAAAGTTTTATTTCTAAAAAAGAAAAAGAAAGAAA AAATTTAAAGGGTGACTTATATCCACACTGCACACTGCCCTTATGCTTATTTGTTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATTC GAGAAACTTCTTTAAACCTCACCCTTGTGGGGTTTGGAGAGGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTATCTTCTGACTGCAAAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAACTTTCCAGGAACACAGTGACCATAATTTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGTGATATGGATACCTTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG CTATTCCCTGIGGTTTTTAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACCCACCACACACCTCCACCTCCAGCCAGACAAAGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGGAGGTGTCAGCCGTGTATCATCGGAGGCGCCGGG CACATGGCAGGATGAGGGAAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAI1	100 A G ---	---	

					CTCTTCAGGAACCAACCAAGTCTTCTTACCAACACGAGCTTATTGCTGTCCGAGAGGTACAAACCCGTAGA	
ESTD-PAR	120	A	---	---	ACTTCTTCCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT	
ESTD- Per/RDS	74	A	G	---	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTCCTTCACTTTCTGTGTTCTAGAACGTTTTCTTAG GACTGGCAGTTTAAGCTTTCACITTAGGCTTCTGTATACCCATGCC	
EST68308	5	29	C	T	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGAGGGCTGGCTG CTGGAGA/JGAGCGTGGCGGAGACCTGGAAGGCTT
EST54045	6	39	A	G	---	GGAAAGAGATTAAAGAGCTTGATTTGGA/C/TAATCTCGTTCCTTTGAGTGTGGAAGAGTTTCATGTC TCTGCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAAGAAAGTAGTATTTTTA
					GGAAATTTAAAAATATTTAAAAATACCTCCATTTTGCCTT/A/GTTCCTTTTAGTGAAGATGATACCTGTC AAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGCCTTGGAAITGGATTTTAAATGTTGACTTTATCAT	
ESTD- PXMP1	88	A	G	---	ATGAAACATGGTCTTTAATTTATGATAATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAA/A/GJAGCGAGCTGTGGTGACAAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAGTCTTATGAAATTTATAATCTT	
					CCCGAGGAATCTGAGAGCGAGCGAGGGCTGGCTGTGGAGAAGAGCGTCCCGGAGACCTGGAAGG CCTTCTGAGAGTGTGAAGAACTGGCAAGGCAAGGCAACAGGTGGAAGCCGAGGCGCAGACGCGAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA	
ESTD-RDS	127	A	---	---	TTGGGAAGTTAGAGCCATATTTAAATTACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCAGTTTCAGTT/C/G/CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT	
ESTD- s14544	94	G	T	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTGGGAGAGATGG/A/C/JTGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG	
EST52908	0	45	A	C	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT/C/JJGGCTCAG GATGCCGGAAAAATGAC
EST19590	55	C	T	---	TGAAGCTTCTGCCAGCTTGCAATTGTTTCTAGGAGAACCC/C/JGCGTACATACCTTTATCTATAGCCTT CCCCTAGGTCTT	
EST76136	39	C	T	---	TGAAACACCTGTGGTCCGGAGCCAGGTGTGTTTCTCTGGAGCCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACCTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACA/C/JCCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCAAAGCCAGTTTCTTAGCAAGGGCAGGAC	
ESTD- SPTB	176	C	T	---		

ESTD-TAT	224 C	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCAATTCATCAGGGCCATCAGTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATTCATCTTTAAATGACTTGTGGACAGGATCA ATTTCCCTCACCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGGATATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THR	125 A C	---	---	---	TGCGGCTTTCTCCGGGAGGTAGACTCTTACTTGGCTGTGATTTCCAAAGAGAAGAGTCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC[A/C]TTCAT CCACACTGGATTGGCCAAACAAGTCTGAGTGGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTCACTCCTGTGAGCTTCTGGATTTCTTCCACCGCAACAAGAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAG[GTAT]CCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGTCAATAATAATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTCAATTTGGCCATAGGTCCCTATGGGATGACA
ESTD-TYR	122 G T	---	---	---	AGTAGTGGATGAAGCTAACCGCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCAATTAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATCTGATTTTCTTTCACGTTTATACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	---	AGTAGTGGATGAAGCTAACCGCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCAATTAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATCTGATTTTCTTTCACGTTTATACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTAAGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T	---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTAAGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T	---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCCCGTTATATGTAAGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC
0			CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCAC/GJTGCGCGGGATGGCCGGGAGTTTC
			TGGTTGCGGCCACGGCTGTGGCTCTGTTGTGAACGGTAGCCTTTCGGTTGGATGCCTAAACCTTTGT
			TTCTTGGCCAAAGGAGGGGGTGCATGCCTGAGATGATAGTGGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTTG
			TCCCTAGAGTCTG
			AGCACCTCTCAGCTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA
EST71770			CATCTCTCCATGAAGAGCACAGAGATTATTTTCTGAAGTCCGGATCTATGACTCAGGGACAT
6	189 C G ---	---	ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGATCCAG/CJTGTTGGTGGGA
			AGGAGTGCCAGTCCCAGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
			TTCTGCATCTCTGTGGAAGTTAGAAGGAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG
ESTD-TNFab	152 A G ---	---	CAATAGGTTTGAAGGCGCATGAGGACGGGTTTCAGCCTCCAGGTCCTACACACAAATCAGTCAGTG
			GCCCAGAAGACCCCTC/GJGAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATG
			CTTGTTGTCCCAACTTCCAAATCCCGCCCGCGATGG
ESTD-TNFa	88 A ---	---	TTCTGCATCTCTGTGGAAGTTAGAAGGAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG
			CAATAGGTTTGAAGGCGCATGAGGACGGGTTTCAGCCTCCAGGTCCTACACACAAATCAGTCAGTG
			GCCCAGAAGACCCCTCAGAAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT
			GTGTGCCCCAACTTCCAAATCCCGCCCGCGATGG
EST52418			CAAAATACAGGGTCAACTGCTATGATGTGTTGGAGCCAGTCACCTTTGGTGGCTACAAGATGTCG
6	113 A G ---	---	GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACT/GJAAGTGAAAACTGTGAGTG
			TGG
			CCCACCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA
EST13586			CCAGTGAGCAGCAACAGGGCC/GJGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA
3	89 A G ---	---	CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGGAGAAAGGAGGTGCTGCTGCTGCC
			CCGGTCACTC
			AGGCAGAACTGGGCCCCCATCGGGGGACGTGGAAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA
EST51976			GGGACAAGGTCAACTCTTCTCAGCACCTCAAGGAGAAAGAGAGCCAGGACAAG/ATJCTCTCTC
7	123 A T ---	---	CCTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGTGCAGATGCTG
			GCCCCCTTGGAGAGCTGAGCTGCCCTGGTGC
			CCACTTTGGTAGTCCAGTGTGACTCATCCACAATGATTTTCCAGTGTCTATCTGTTCTCGAGTTT
			CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTACCATTTTCCACAGTGGT
EST11458			CCC/GJTTAAAAACATTCATGAGCCAGGAGAAGATACGTATTCTCTCAAGCCGGGCTATGTG
6	140 A G ---	---	TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60	C T	---			AGACCTCAGTTTCCCTCTCTGTAAAGGGGAAGTTTGTTCCTGGATCTCCATGGGCCCCAGC/C/TAGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106	C G	---			CGGTCTCTCCAGGTATTGTGCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCATTAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTT/C/G/GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCCTGTTCCAGTGTAAAGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G	---			ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTGGGGCCCGTGG TCTCTCTGGTGTGGGTAGTCTGGAGTCAACGGTGTCTCTT/G/GTGAAGCTGGTCTGTGATGGCA ACCTGGGAACGATGGTCCCCAGGTCCCGATGGTCAACCCGGACACAAAGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120	A C	---			AGTGACTTCAAGGAAATGGCTACCCAACTTGCTTCATGGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTGATCATATGGATGAGGAGACTGG/C/AACCTGAAAA AGGCTGTCAITCTACAGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATAGTGGCTGCTCTAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112	A G	---			AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCCTGCTACTT/C/A/GGGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCCTATTGAGCTGTAATACCATACCGTACCT
ESTD- COL2A1dd	97	C T	---			TGAGAGAACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGACCTGGAACA/C/T/TGGACTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAAATTTTATTTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150	A G	---			GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGCCCTAGAAGACATGTTTGTAGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCCCTCATCATGAAAC TGGGAGGCCCGGCAT/C/G/GTGTCTCATGCTGTAATCCAGCATTTTGAGAGGCTGAGGGGGTGGAT CACTTGAGGTGAGGAGTTTGAGACCAACCTGGCCAAAT
EST12274 0	135	A G	---			CCCCAGTTGACAGCCACTGCTTAGACTAAGTTTCTTCTCCAAATAGAGCCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCTCATGACCAAAATATCTTCCCTCTTAGGATGAGGTG A/GTATGTAATGACCGATGGGGTCAGAACTGTCTCTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCAGATC
EST76807	91	G	---			ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTAGCCGATTGTCTATCTCCAGCGGCCCTGTATC CAGCTCACTCATCAATGGGGCCAGTCAAGGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---			TTCACTTTGTGGATTGTTCTTTTGTGCTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCCTGTGCTTTGTGGGATATTTGAAAGAGATGCTTTTGCCAGTCCAATGTCCTAGA GAGTTTTCCCAATGTTTTCTTGTAAATAGTTTCATAGTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTGATTCTGTGA
ESTD-RYR1	109 A G ---			CTTCGTACGGGAGGTACGTCCTCCGCCCTCTTCATGGACATATGGATGATGTGTCGACCATTTCCOC CTGCTGACAGTGATGACACGCGAGACTTGTCTACTATAGAGAGGGGAGCTGTGTGCACTCATGCC CGTCCCTCTGAGGCTGGAGCCACTGAGAACTAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---			AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCCTGCAGGATGTG CGIAGTCGTGTCCTGGAGTAGCCCCGACTCTTGTACGTCGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C ---			GATAAGTACACTGAGGCCCCAGGAGGTTATTGCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCCGTAGGGAACTGGGGGATCTAGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGCTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGAGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---			GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGCTCCGACCTAAGCGGAGCAGCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	122 A G ---			CCTTCTATGCCAGATGGAATTCAGTCCCTTCCAGTCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAGGGCAGGACTAATCCAA[AG/TC]CTCTACCCGAGCTTGTGCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---			TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[AG/TC]CAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAATGATTACTTGAAGGAAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTACTTATGAAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---			ATGGCTTGCCTTGGATTTACGGGCGCACAAAGGCTCAGCTGAACCTGGCT[AG/CC]AGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCCTGCTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCTCGCCAGCTTGTGTGAGTATGCTATCCAGGCAAGCCAC
EST54419 8	88 A G ---			GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGAGTACAGGATCTGCQ[CTGTCTCCCTGCTGGGGGGCCCAACCCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGCTCCACTCTGAACATCTGCACAAAATCGGCCTGC CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCATTATTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTAC[AG/AT]CCTGGGAGATGATTTGGGTTTAGCGTGTGCTATGTTGCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGAGTAAACCTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAACCATAGCCTA/GJTTCGTAGCCATAATTAATGGTTGTGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAATCTCCATCACCCTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGAGGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTCTGGCCACC GTGGGAGGCAACCTGCTGGTCACTGTGGCCATGCCCTGAGACTCCGAGACTCCAGACCATTGACCAA CGTGTTCGTGACTTCGTGGCCGAGCCGACCTGGTGATGGGACTCCTGGTGGCGCGCGGGGCCA CCTTGGGCG
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTGCTGCTGCCCTGGTTC/GJAGCCCTCATCTCTTTTA CAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGCTCTCTCCCAATCCATTCTTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATTCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 GT ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JTAGATGG TATTGGAGAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 GT ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JTAGATGG TATTGGAGAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACATTTTCTCTAATTAATTTACATTAGTCTCATTATTCTGAAATATTAT TTTTTACA/GJTACCCCTTGTATTATTTTGTATTCAATTTGTACGAGAGATTACAATATCAGTAACGC TGTTCAATGATAGTGCATACAAATGTCTAAATACATTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGTCTTATGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATGCTTGATGAGCCTCT CAA/CJTTCCTTAAGTGTGCTGCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCATTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACATACATATAAGAGAGACCTGTACCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAAGCAGCAAGGAGAGAAAGGAAGT

WI-2625	98	G A	---				GGCAGTCCTGGCTAGTGGTAGACAGCACTGAAGGATGGAGGAAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAAGGCTATTTAGGA[G/A]CAAAATGATGATACCTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54	G A	TAGG	GTCTCTCTTA	GCCTAAGTGT	AATCACAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCTCTTAGTCTTCTTATAGG[G/A]ACCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAACAAATC
WI-2939	72	G T	GTGCCITT	GGCTTGCTCA	CTTGTTGAGGG	AAGGTCITG	CCATTGTTGAGTTGGTGGGGTCACTTGTCAATCCCTCGCACTCAACAAAGTGGCTTGCTCAGTGC CTTT[G/T]CAAGAACCTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGAAAAACICAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99	G A	AGACGAG	GGTTATGCCGC	TCAAGTATTGC	CTTGTTGGG	CTTGCTACCATGCAATTCACAGCATACAAACCTCAGTGAATGCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAAGATTTGGATGGATGAAAGCAGAGGAGATGCTAAAAGTGA
WI-3473	101	A G	GCCCTAGGGA	AAGCATTTTA	CCTGATGTCAC	CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGGCCCTGTTTGG GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796b	29	A G	---		---		ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTGGCTCCCC
WI-1796	29	A G	---		---		AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTAGGTATTTCCAAATAA[C/T]AAATGCCCTCTGAAAAATATCTCTCCCATGTCCCTGTCT TAAATATAACATTTTCCC
WI-4360	93	C T	AAATAA	GTAGTCACATT	GAGAGATATTT	TTT	GCTGAGCTTTTGGCAGAGCCAGGACAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACCTGAGAGTGGTTTTACACCCAAA
WI-1959b	87	C T	---		---		GTTGTGCTGTAGCAGACACAGAAAGGCA[G/A]GAGAGGAAAAAGCCTTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAAAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28	A G	---		---		CTTGAGTATCGCTGGATTTGGTATACACAGAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAAATGTATCTGTTCTACAATTTACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATTT TACTGAGCTGTTACTAGGTGGCTATAAATAGC
WI-1980b	140	C T	---		---		

WI-2015b	190 A G ---				TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAATTACTTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACCTA/GC/CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---				GAAGGCACAGGGAAGATGGCTGTCACTACCCAGCCAGGAGAGAAGC/C/TACATTTATTGGTAA TCCTATAAGTGCACTCTTAAATTTGATTTACTTTAGA
WI-754	22 T C ---				GAAGGCACAGGGAAGATGGCT/C/GTCATCTACCCAGCCAGGAGAGAAGCCACATTTATTGGTAA TCCTATAAGTGCACTCTTAAATTTGATTTACTTTAGA
WIR-1b	56 A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAACTCTGATCGTACATCC[A/G]TGGCGTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAACTCTGATCGTACATCC[A/G]TGGCGTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---				TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAGTTATTAGCTCAGAGCCTCACACATTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---				TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GA[A/G]TATCTAAAGTTATTAGCTCAGAGCCTCACACATTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---				GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C ---				CGGCACAGAGACAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---				CGGCACAGAGACAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---				CGGCACAGAGACAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5e	177 C	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGT AGGTTTGAAGGGAAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACAC AGGTTTACGTCAG
WIR-6	63 A	C	---	TAACCCCTGAAACTTTGTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AVC] CGCAGCTCTGGGGTGGGCGAG
WIR-7	12 C	T	---	TTGCTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGICTTGAGATTGATC
WIR-8	46 C	T	---	GGCGTCCTATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-2	56 C	G	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAAGTTGTGAGAAAGGATGATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G	A	---	TGTCCTTGCTTATGCCTGCTCTTTCGCTTGGCAGGATGATGCTGCTAGTATTTCACAAGAAAGTA GCCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTCTAGACTCAGCTGTTCTCACTC
WI-18694	41 A	T	---	GGTCATTTCTTTTATCTGTCAGGCAGCCAGCTCTGACTTTA/TCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCACCATGATGATTATACCAATAATACAGTTCCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAAATGCATAATCTCTGAAAATTATGAAAACATCCCT

WI-18517	87	C T	CAGGAAATCAG GTGCAACA	TGTTTGACAA GTGCAACA	TAAATAATCAACTAGGGCTACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCGACGCTGTGTGCACTGTGCCAAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA GC	GCTAAATTA CTGCACITTTT GC	CGATTGACAAACCTTTTATTTTCAACTTAGGTAACTAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAAAACGAGCAAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75	T C	AGCATCTGGA TACAACGGAGC	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAATTCGCTCCGTTGTATATTCAGGAGGGA
WI-18704	99	A C	GGGTTCTCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACCAACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCGAGGGGTACAC/C/CAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAAAACCTTGTTTTAAATTGCAAAACAGTAAATTTACAGCACATTCATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTOGTGGGTG G33G	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAGGTCGTGGGGTGGGGGTGCAGAGTC/C/GTGTCTCTTC AGTGGTATTGGGACC
WI-18533b	91	T C	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTCATCCTAAATTC/TACTGAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTCTTTA TTTTATATTTTCATTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTTCAGAT TTC	AACCAGGATA AGGCTACAAGT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTTCAGATTTTC/C/AAATAGTTGTAGCCTTATCCTGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGAGCACAGCTCATGGGCAACATCATCTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATAGGGGCTTTTCATGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTTAT/GCCCTGGCCTGAAAGTGGCCCATCATACCCACTGTT CT
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCCTTC/CATCCATCCACCACCTGCTGATTG
EST10052 2	24	G A	GAGGCTG TC	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTGAGAGTGAAGTCAAGATTGAGGTTCCACATCTTGTGAGGGCTTC CTGTTGAGTCAATCAACCTGGTGGAGTTCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---				CTTGCCTAAATCACAGTCTGTATTATACAAAAACCTTTGTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGGAGATGCCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G TAATCT	CTCTCAAGTAG ATAAGAGGCA			CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAAATCTTCTGAAAAATTTAGCTTATGAACCTATTACACTGCAAAACCAGAGAAGGAGCAC
EST11260 8	101 G T ---				TATGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGTGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---				TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCAACAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGATTGAGCTTTACCGCTTTCTCTCATCTGCTGGTG[C/T]TTCTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI. 16632a	71 A G TGGAGCCT	CCAACCTACTT			GAATCTGGGTATTAATAGCGGTGCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[G/JAGGAGTTTATAGAAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGGA
EST11772 6	74 A G ---				CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[G/JGACTATTTTCACTCTGACTATAAGTGAATAAATACATTTGAAGACTTTCAGGAGCTCA
EST11795 3	82 G A ---				CTTGCTCATTATTTTGTGCATGTGTTCTTAAAGGCTTGTAAGATAACTTGAATGTGGGAAC ACATAGATCCCA[G/JATTTAAAGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT			AGAGCAATGGTGGATCTCAATAAGCAGCTCATTTTGATTAC[G/JGGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCTCCACAGAACTTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G CAAAGTCTGT	TTGTATAATA ACACTCAGTA			GCCTAGTAATTCAAAAAGAACATGTTTGATAATAACACTCAGTACAAAGTCTGT[G/JATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ---				GTGGAATAATTTTATCTGTACGTCTTCC[T/C]ATTATAATTATCTTGCTCTTGAATTCAGCACCC CACCCGATTTGACGGCAGTCTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT
EST12492 1b	95 A G ---				CCCTAGCAAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTGGCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[G/JGGAAACGCACAGCAAAATTGACGATGCAGCTTTTTA CCTTTT
EST12492 4	25 A G ---				ATCTTGAGGTTTCTGGCCTGTGAG[G/JAAGTGACATCTTTTACTTACCACAGGTGAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAAACCAACTGGAGGCAAGTCCACAGGTCACACTTGTCAIC/G/CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTACGGGGAAATGACCAATTTTAAGGGCCATGTG GTCGCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACTGTCAAAA CAGGTGTTTTATTATCCCAATGACAGTGTTCCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCATTATTCAATTTGTTCAAAACACTGTGTAGTACCAACATTGTCCACCGGC(A /GTTGAGAATACAATATTGAAGAAGAGTCACIGCCCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TGGGGTTCTCCAGGATTCCAG(CA)CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGATGGGAATCCATGTTCGTTGGTACTCCATCAGGTTCATGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA/T/A)CAACAGCCCAAGTTATTTACCAGAAATTTGTTTGGTTTCA ATGATGTTTAGCTTTAATACACTGCACCTGTTTIG
EST12949 2a	52 A G A T A C T G T T GGCTTTAATCA TAACCTAATA			AGGATTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC(A/G)TCTGTCACTTG CAGAGACCCACAGGGACACACATTCCTCTCCATACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAAATGAAGCATAATAAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA(C/T)GGAGCAGAAAGCAGCTTCCCACCCAAG CACTCTGAACT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTTAAAAATTTAATCGCTTTATACAAATTGACACCAAAATAAATGCAC(A /G)TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC(C/TA)GTCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCGCAGGCCAGTCTCTCACTGTCCCATGAATAGCC AGTCTATTCTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT(T/G)GACTAACAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC GCTCAGATGTG ACAGAGA			GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTCCGCTCAATATGAGGCTCAGATGTGAGAG ACGC(GA)TCTCTGTACAGGAGCGGTACTGTCTTCAATCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCCT AACCAGATTT TGACAAAAGA G			AAAGATATAAAACAACCTCCCATCAGTAGCAATACAGGTTATACATTTTAACCAGATTTTCTCAGG CCTT(C/TTTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCCTCTTGTATATAACCA

EST13278 2a	51 A G G	CTTTCACCGAA CAATATTTTAG G	CATATCTTGG GTGGTGAGAA	TTTCGCAAGACGTTTACAAGCTCCAAACCTTTTACCAGAACATATTTTATTTAGG[A/G]ATTTTGAAATTTAT TTCTGTAGTTCTCACCACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTT AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAATATTTAGATAATACCTGTGGGAAAGTGTGAATTTACTAGCC TGCCTGAGAATCCACACATTTTCAGTCCAAGA[A/T]AACCTTCTCTCAAAATTTTCCATCTCCCATCAGA GG
EST13290 9		CAATTTTTAGA AGTTGGGTTT	AAATCAGTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTTTT TTTCTGTGCTTAACCTTACGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGGGGCTTTTTTG
EST13518 2	45 C G		---	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCATT[A/C]GACITTTAAAAATTACCTCA ATGTTCTCGGAGTGTCCATAGTTTAAATGACITTCGACCTTCTTTAACTTGATTG
EST13522 8a	66 A G		---	CAGGTTGGTATTCTCAACTAGGAGCTATTTTGCCCCCATCCCCCAGCGCAGTGTCTGGAGAC[A/ G]GTTTGTATTGTCACAACTGCGAGAGGTGGTGTCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGAGAAAGGAGGTTGGTTAGTTGAGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCAATAAGAACTGCCCCCGACCCATACACACAAATTTATAGCAGGTAAAAACCAA CTGAAAGGAACAAAGTAATGACTTCTTGAACAA[A/C]GTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCTCAACCATCTGTAACCCGAGCC[A/G]CAGTGACCGGACTTGCTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATCAAAAGTTAAAAATATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAAATATTTT AAAAGA	AATATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATT[A/T]CTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCCCTTCACACTCATTTTTAAATTGT
EST14812 2	50 A G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTAC TTAAATCCCAT TAATGACT	TTTTCATATGGGTGATT TTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCACAC ATACTGGTT	CGGGAACA GTACCGGAA	TTTGTCTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGCGCGTCTCCCGACTGAACCCAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAAGTTCGCGGTATCACCCACCACTACTGGTT[A/T]TTC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---	---	---	TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCATATATCATATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	---	---	GTCACCAAGCACTTTTATTAAGACGTAAGGAGCAACAGAGAGGA[G/C]AGCAGAGAAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	---	---	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGTTTGGCCATCACAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	---	---	CTTCTCCTTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTTGTGGGG
WI-16783	64 A G G	---	---	AAAAATGTAAACCTTAGAGGTTGCCCTCTTTTGTCACATTTTCTGAGATGCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C ---	---	---	CAGGACTTAAGGTCTTTTGGCTGGAAGACTTTAACTAAAGTCAAGGCAACATAGGAT[C/T]GTGA CAGCAACACTCGGACCAGGAAGTGTGAAATCGTCACTAGCGTGGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---	---	---	GGTTTGAAGACGCGAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGACGC TTTTCAGAAAGGCGCTC[G/C]GGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---	---	---	CGTCTGAAGTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTC[C/T]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---	---	---	ATCCAGCTGTGAAGGACAGAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTCACATCCCA GGGCTCCAATAATGCAACATTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---	---	---	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCCAGGGA[A/G]TTGGCCCCGAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	---	ATGGTATAACAAAATCAGTCCAGGTTTTCCTGAAACAAATGATCCTTTGGCTTTCCCGTGGC CTCCTAAACAACTAAACAAACCCCTCTACGCTCTAATCAGTCACCTTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---	---	---	ATGGTATAACAAAATCAGTCCAGGTTTTCCTGAAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTCTACGCTCTAATCAGTCACCTTAAGATAATCGAGTGGCAAGT CTTTCACA

EST16151 2	53	C T	---	AGCCAAATCAAACGAACCTATCAAAAACACACAAAGGCCCTAGAGGAGAGATTAC/TAATGAACGCT AAATAATTCAAGGCCAAATTTTGATCTAAAGCAATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54	G A	---	CATTGGTTGGTAGGGAAGATAGTAGTGCAAAATAAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59	A G	---	GCAGGTAACCTGGTTCAACACGTAATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGCTTCTCGCCCTTCTTCGTTTCATAATTTTATGTCACGTGCTCTAACGTGGGCCGCTGT GCAAGAGATCTTTGAGA
EST16198 4a	28	G A	---	AATCTTAGGCTCTTGGCTTTCAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCAGAGGAAAAGTCAGCATATAAACCCACATGGGTACATGCTCACGCACATGGTGTC
EST16229 2c	52	T C	---	TGTGAACCTCGAATTCGCTTGTCGAAGTCCTGAGTACAGTTTCATT/CJTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45	T C	---	TGTGAACCTCGAATTCGCTTGTCGAAGTCCTGAGTACAGTTTCATT/CJTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124	A G	GGAGCCATTGT TGGGGTTA	CAGACTTTTCTCACAACCTCATTTGGCTGGAACCTGGGTACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGTTCATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49	G A	---	GCCACTCTCCTGTGGCTGCTCTGTCAGCTGCTGCCAGTGCTGCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAAGCATTTAGCCAACTCCTGGTCTGCTCCACTCTCTCTCTCCGCGCTGGGGCTCACACC TCTTCTCTCTCAATC
WI-16824b	83	G A	---	GTCACCCAGCCAAATGCTTCAGGAATAAATGATGGTCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCCTCCATTATGGGAATA
WI-16824a	47	T C	CGAGTGT CAAGTGT	GTCACCCAGCCAAATGCTTCAGGAATAAATGATGGTCTGCAGCTGTT/CJGTTCTTATGAAGAAGTC AGAAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96	T C	---	TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTTCATTACAAA AATGGCTTCCAAACCATTAATAATGAACITTC/[GGAATAAGAGCATAAACCGGAACAGTAACATCA
WI-16857	47	G A	CAAATAAGCA GCTAATGGCA	TATAATCCATCCTCCAACACACACAAAAATAAGCAGCTAATGGCAA[TG/A]CTAGTGGTCTTCCCAA TTCAGAAGACCTGTGCTTCAAATTTGTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79	C T	GATACAGCC ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATATTTCCAGATACAG GCCATATTTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99	A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATCTCCOCTTTCACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGCTCTCTGAC[A/G]GCGATTACCTGACATGTGTCTATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTCACTACCTCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C T	ACTTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTCCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74	G A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTATATTGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACCTTCAATTTGGGCTGAACCAAGTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAATACTACCACTTCTCTCTGCTACCACAGAGCAGCTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACAGCAC[C/T]GATGCCACTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGCTCTCTGAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGCGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCTGGAG[C/G]ACAGG TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGG[A/C]CCA CGGGCAATCAGATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAAT[C/T]CTTAACTTGGTCCAACATATT AGTATAACTAATAGATTTTATCTACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATT[C/J]ACGGCTGG AAATCAACATGCCTCTTCTCTGTGAAGTTGTCAGCATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGCGCCTCATCTGAGAT[G/G]TG TAGGACTGAAGGAATGTTTGGGGTTTAGGAA
WI-16992a	46	G A TC	AAGCACCCAG AAGTACACTG	CACATTCCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGT[C/G]CCCTCATCTGAGATGTG TAGGACTGAAGGAATGTTTGGGGTTTAGGAA

WI-17010	23 T C	T T C A A C A G G A	A A T A A T A C G G T	A T G T T T C A A C A G G A A A G C C A T G T C J A T G A C A T T C A A A C A C C G T A T T A T T A G A A G C T C A T T A A T
EST17127				T G T T T A A T G C A G A C A A A A A T C A A G G T A A C T A A A A G C A G A T C C A A T G A C C C A G T A T C A A C C T A G A
9b	74 C T	C A C T C G G C A C	G G G A G G G C A G G	G G T T C C C A C G
		A A T T C T C T T A T	G G T G	A T T C G T C T C A A A C A G C A T C C C A G G C G G G C A T C T C C C C A C G A T T T T A T A T A C A C T C G G C A C A G A
WI-17040	94 T C A	C A T C T C A A G C C	G	C A G A G T C J T T G G G A G C C A T G G G C A C C C C T G C C C T C C C C A G G C T T C C T A A G T A A C A A C T
		G C C A A G G G A T		C A C G G T T C A T T A A A T T G G T A C A A A G C A T G A A C A C T G A A C A C T A C T G A A T A A G C C A T A G T C C C A G T C T C G T T T C C
		T A A C G T A T A G		G A G A A T T C T T A T C A T C T C A A G C C A G T J C J A T C A C T G A T G A A T A A G C C A T A G T C C C A G T C T C G T T T C C
WI-17044	47 G T G	T A A C G T A T A G	G G G A T C C C C T	A A A T C T T T C T C A T A T T G T
		T G G A C T T G T C A	T G T T A A G A	T T G T T T G T T T G T T T T C C T C C T G C C A A G G G A T T A A C G T A T A G G J G J T T C T T A A A C A A G G G G A T C
WI-17021	62 T A A C T C	G C C T A T A A C T		C C C C A C T T A T A G C T G A C A G C A G C T G C A A C C A C T G A C T C T C C T G C A G A A T G G C A G G A A T C G A A T
		A A C T C		C A A A A G A A A A G C A A G T G
		T G G A C T T G T C A		G C A T G T T G G A G C A G A T C T C C A T G T A A G C C A A A A G T G G A C T T G T C A G C C T A T A A C T A C T C T J A G
WI-17065	90 T C C T T	A A A G C A T A A A	T G T A G A G T T A G	C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A G C A C A T G C C A A A G T G C C T G G
		A A T G A A A T C C T	T G C A G C T G C	G A G T G C C A A T A A A A T C A A
WI-17066	32 A C T	T G T A C A G C C A		
		A C A T C A C T G T T		T G T A A A A A A T G T A G A C A T G G G G G A A A A A A C A T T C G T A A T C A A C A T G T G T T T T C T A C T T C C G G T A
				C C A G A A A G G A
				T T C A T A A G G T T G T A C A G C C A A C A T C A C T G T T J A C J A T T C C A G A A C A T T T T C A A C A T C T C A A A A A G A
				A A C T C T G C A C C C A T T A G C A G T C A T T C C C T G T A G C T T C C C T C A T A G G C A A T G G C A A C T G C T G A T C
WI-17074	86 T G ---			
WI-17104b	108 T C ---			T G C T G A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T C A A C T G T T C C A A G C A T
				A A C C T C C T A C A C A G G C C T J G J C T A C A T A G G A G T A T A T T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
WI-17114a	37 T C	T T T C C A T C A A G		C A G A T G A G A A C T C A T G C T G G C T C A T C T G C A A G C T T C C T G A T G C T T T G C G A G C T T C C C A T T C A T T C C A
		G A C T T T G T T T		A A T C A G A A G C A G T C A G T G G C C C G T G G T T C C A G A C G G C T J C J T C T C T T T G T T A A G A A A T T A
				A G C G T C C A A C A G A T G T T C C A T C A A G G A C T T T G T T T J C J G T C T C T T C A C T C T G C T A T T T A T A A T A C
WI-17114a	37 T C	G A T G A A A T T C		A A G C T A C C T C C C A A G G C C A G A T G C T A A G T G C T A A A A G A A G A C T G C A G C C A C A A T C A G A G T T A C A T
		A G A T A G T C T T C		G G G A
WI-17150	76 T G C T C T			
		C A T T T C T T T G T		C G T G G C T G G A C T A A G T G C T C T T T C C A T G T G G A C A C A T C T C C A C T G A A C A G G A T G A A A T T C A G A T A G T C
		A A A A T A A C A A		T T C C T C T T J G J C A T A T C T C C A G G A T T C T G A A G G G C C C T C C T T T G T C T G C T C T A A T T T
		T A A C G A T C T T G C		G A A A T C G A A T A C G T C C A T T C T T T G T A A A A T A A C A A T A A C G T T J A G J A A G G C A A A A G C A A G A A T T C T G
WI-17163	43 A G T A A C G T T			T A A C C A A C A T T G G A A A A G G G C A C A G G G A G G G G C A G A G G G A A A G G G C A G A T T T T C A A C G G T T T
				C C T C C A C A T C T G C A G A C A A A

WI-17178	127	T C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAATGTCCTCCCAATTCATTAGCTATGATGGAGTTATCAGTTTCAATTCAGAGCGAAATTACTGG GGCGAGGGGGTTTAATATCCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTCJAGAA GCAGTTGAAAATTGAGGG
WI-17180b	81	C G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAACTCCTGCACCTCCCAAGTCTCGTCGCACAG GCTTCAACAAATTACIC/GJAACATCTTGCCCATTTTGTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T C	CACAAAAATA TAGAGAATCC TGCA	TGGCAGGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAACTCCTGCACCTTCJCCCAAGTCTCGTCGCA CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATGCTTCCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79	T C	CAGGCAGTTAATGTGCTGACATAGTAAACAGGTTTGAAGGAGGAAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCACTTCIGTGTATGAACATAACAAAGGATGGGAAAGAACACATTTCTCTCACA
WI-17149a	48	C G	CAAGTTTGA AGGAGGAACA	CCACGCAOCTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAAACAGGTTTGAAGGAGGAAACATCTCATGCACGTGCGTGG GAAACCCAAATTGTCATGTGTATGAACATACAAAGGATGGGAAAGAACACATTTCTCTCACA
WI-17197	67	G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGTGGT GCATACC	ATTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCTCCTGCCTCAGCAGAAAGTAGCTGGGGCTACIG /AJGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAATAGAATATTTGACTTTTAGATGCGCA TGATTTTCAGTACTTTTCTCCCTGCTCCCTAGTTTTCJTAATTTCTCAGTGGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
WI-17198	38	A C	TCCCCTTGTC CCTAGTTT	TCCATTTGTCC ACTGAGAAAT	TCGCTATGCTACCCAGGCTGGTCTCATTCJTCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACACAACCTGCCACCGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
EST18753	27	C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TTATTTTAAACATAACCCAGATGCACCTTGGTTTTTACATCTCTGTTGCCATTCAGTCTCAAAGT AAACACICJTGAGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT
WI-17108b	74	C T	GCCATTCAGTC TCAAAGTAAA TCA	AACTACGATTT ATCATATGCTC CC	ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCAJGJTGCGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTCAATCCATCCCGTT
EST19067	41	A G	ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCAJGJTGCGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTCAATCCATCCCGTT
EST19067	40	A C	CGTGACCATT AAGGGTATAG TTC	AAAAGTTGAA TGACTTTAATG CCA	ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCAJGJTGCGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTCAATCCATCCCGTT
EST19125	28	A G	CTGTTTCTCAGAGATGACACTGCCAACA/JGJTCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTACAGTAGTGTGTTTTTCTCTGAAAAA

EST20824 8	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAGCCGGAGTTTATTATTATTAATCAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCTCAGAACTTCAGCCCT[A/G]GTAGCACAAGTGG ATGCTTGAAGAAACTAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTAGTGGGACCA
EST21904 b	128	G A	TTTCATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCGAGTTTTCAGTGAGGAGCAGAGGAAAGTAGACGAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T C	GAAGATCTGT CTGGCATTTCT	TGGAATAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATCTTTT[C/G]TGGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78	T C	AATTATTCTGC TATTCCTGCOA	ACCATGAAGG ATGCGGT	GTTTAAATGATCACTACCCAAATCCACAGAGAGATCTTAAATGTTTACAAGCACCAATTAATCTGCT ATTCTGCCAATTCACCCGCATCCTTCATGTTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92	T C	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTTACTCTA[T/C]TGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54	A G	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCAGTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41	T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATAT[C/J]ACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19	A C	---	---	TCGAGGAGCTCTGAGGAGC[C/J]CACCAAGGGACGTGTGCCAGGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCTCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGGCCTTCT TAAGCCTTTTTTAAGTGT
EST22433 c	103	A G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAAGTACAGAT AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATCCAGGTACACATGGAAGAACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTGCTAAGCTGAAGCTGAAATTT CTGGGAGCTTGACATGCTG
EST22657 9	71	A G	AAATGGATCC TTATCTGCACA	GCATGAATTTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAAATACAATTTCTATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTGTT TG	TTGCCTGTTAA TTTGACTGTAA TG	GCCTTTTATTGCTCTCTTTAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTTCTACCCCCA ATTC/CATTACAGTCAAAATTAACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCATTGTTGACTTATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTATCTTTGCCCTTTT/AJATGGTTTTGACAGTTTGTGTCTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTCTTAGGCAAAAGCCATTTCTTTG
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAAA	GCITTTGCCTA AGATTAATAGT AACTACT	TTTTTGGCTTGCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCAGCTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGCCTGGCTCACTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCOC TGTAAGC	AAAGGCTGTTAGTTTTGTTTTGTTTTTCCCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCGCCGAGAGAGAGGCTCAGAGATTTCTAGAGGCGGC TGAAGAATACCCACCTAAA
EST23733 9	31 T G	GGCTGTTAGTT TTGTTTTGTTT	TGCACITTTAAA TCCCATCAAT	CTGACAGTCCCTGTGTGCGGGGTGTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGGCCCTA/GJTCGGCCTCGTCACTGGCCTTGTCTACTTTGTATTTCTGTCTTGGTTGAAA TACCATCAGCCTTCC
WI-17470	83 A G	GTGTCCTAGC TAATGAATGC	CCAGTGAAGAG GOOGA	TTTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTTCTATTTTAAAGCTTAGAACAGTACATGGTGATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCAAGTTTGTAAACATTATTCAAGCTTCAAGCTTCAAGTTTGTATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAACCAAGTTTGTAAACATTATTCAAGCTTCAAGCTTCAAGTTTGTATAT TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGGCGCAATTTACATTGACGCGTCAATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/C/JTAGGGCGCAATTTACATTGACGCGTCAATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGTTGGAGTAGGAGAGGCGCTACT TCCTTGTGTAAACACTCCC/C/GJATATTGTGCGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTC

WI-17623	46 T C ---			---	TGTGGTTTAAATTTCCATATAATAATAGTGGGGCACATTTC/GCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAATCTTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---			---	ATTTACATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/TTC/GGGCAGTCCAACTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG		ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGCCC	ATTTACATACAGAGATACAAAGGCAACTATGTGCAGC/AJACAATCTGATGGCAGTCCAACTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ---			---	TCAGCTTTAAATTTAAGGGACATGTAATAAATAAGATGCATTTGACAGGACAGCAGACTAGTTC AAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAAGTGTCTGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			---	TACTTCAGTTTAAGGCAAAATTCACACAGAGACTGTCTC/A/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCACATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---			---	CAAAGGATTTATTTTGTCCCTAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATCTAAACATTTTCAATCATCTCTCTCTC/TJTTACATGGTGACTCTTTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33 G A ATTT		GCACTTTGCAA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAAT G	TTTTTGCACTTTGCAACAATTTAATAATTTATC/GA/CATTACAGTAGCATCACACCAGAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTCAGTATTTCTGTACACATCTGTTAACAAAGAACCCCATACATT GGTAAATTCATTTCT
EST27662 4	51 C T CTCCAGTCTG C		CACATTCTGTT CTCCAGTCTG	TTATGGAAATG GCTTATGTAAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTGC/TAGGTTACATAAG CCATTTCCATAAATTTCTATAGCCTTCTCTTAGAGTAACACACACACTCTTTGTTAGGAATGTTT
EST27788 3	100 A G ---			---	ATTTTATTAGGCGGTACAATTCGAAGGTGTAAGGTAAGGGAAGGGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACATTTACATTTCAAGGAC/A/GJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGGAT
EST27828 4	58 G A AGAACCCAC		GGAAGTCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCCTTAAAACCTTCTCTTCTGTTGGATCCAGTGACGTGGAAGTCATCAGAACCCACAG/AJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC		AATAAATTC AATCTGTCAC ACAATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/G/AJAATG GATAAGGCTTCTTGACAAATTTTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---			---	TCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT/T/CAAAAGAAATGATCAATCTGTTGCCCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGACACACCCAGCCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31	T A	GGAGTAAAG GTGTTCTCT TTAA	TTTCTGCAAT TAATTTATAC CA	CATTGGAGTAAAGGTGTTCTCTTTAAAT/AJATGGTATAAAATAAATCGGAGAAACATTAAC GGAGAAATGTACAGACAACAGACAGACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50	T C	TGGGCGCTCC TGTC	TGGGTGGCAG TGTC	AGAAATGGTCTAGTAATCGTTGAGGATTTGGTGATGGGCGCTCCCTGTCT/CJGGACACTGGCCAACC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGATTAGA
WI-17730b	68	T C	---	---	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGATACACTG TT/CJACATGATTTATGGCTGTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTC
WI-17730a	39	A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGATACATA CTGTTACATGATTTATGGCTGTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTC
EST29041 5b	53	G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACATTAAGCATCATTGTCACTG/AJGCTAACTCCT CAATCAACAATACCCCTTTATTTTAGCCATGAAAAC
EST29128 4	58	A G	---	---	CTTTAGAAAGACACAGTCTGTTGGACTTAGGGCTACCCCTATTCAGCAGGTGCCJ/AJGTTATTT TCACCTGGTTACGTCTGTAGGACCGTTTCCAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTCTGGGGACACT
EST29912 3	103	C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCCTCTG T	ATTATTAGGTATCTGCTGTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCTC/JACAGAAGAATGAGACACTTACGCCATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCCG
EST30223 2	99	A G	---	---	AAATAATACATCATGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTAATATCC/AJGGATTTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86	G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAAATAGGTAGC/GA/ATAACCAGGCTCACTTCCCTTCCGTTGAGAACTTCGTGGGAC
WI-16260a	59	G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGTTACCCC AGAGTTTCAAAATATAGGTAGCGGATAACCAGGCTCACCTTCCCTTCCGTTGAGAACTTCGTGGGAC
WI-17835	30	G A	ACAGGAATA TTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG/AJGCTGTTTCTATACCCCAATATCATAAGAATT GTTGTGCTTCTATAATGTTCAAGCTTCAAAATCTTTTGTAAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCAG CCAACA	CCCAACAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTTGTCAGCCAAACAC/CTGGAGGTGATTTTGGTGGGAATTTCTTATCACAATTATTCT
EST31968 8b	95	T G	---	---	CGAATTTGTCCTCTATTATTGTTGATTTCTAGTAATCCTAAAGATTGGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCAATTT T	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCCTCTATTATTGTTGATTTCTAGTAATCCTAAAGATTGGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAGTGGCACTGATTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACAGCTACCATGCCACATCCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TTTCAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCATTGGGTGTTGCTCTAAGTTTCTGGTCACTGCAGCCCC/AG TTCTGTATTAGGGAGACCCCAAGCCAGTAACAATATGGTTCTTGCAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA T	TTTCCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GAAGACTGGGATTAATTGTAGGAAATATTTACACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGCTG GGATGACTTTC T	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCTCTAAAGCTGGGATGACTTTCCT/G/ATTTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAAATCAGAATCCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTTCAATCT
WI-17860	121	T A	TTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATTTGCTATAAGGAAGGGAAACAAATCTTTA TAGTGTCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA ATTGTT	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTTTGTATAGCCTACTTCTCAAAATTTGTT/A/TTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTACATCACATCACAGTAAACTACCA
EST33301 4c	80	G A	---	---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCTCACACAAGCATGATC AATGCCACGAGAG/G/AJACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCTCACACAAGCAT/G/AJ ATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A CA	AGCGTGGTTTT CAATACTAAA CA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGTCAGCGTGGTTTCAATACTAAACA/G/AJGTGTAACAATGCAAAATATT TAACAATAAATACAGTGAATTAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAATGAACAC(A/G)TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA GAT	AAGTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T(A/G)GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT(C/A)TACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTTAAAGC(C/T)GGAAAGGATTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACCTCCGGTGATAATCTGOCATTTATTGATTATTATTATGATAAAACACCTCTCATTTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCAACCACTGTCCCTGTAAATGT(A/C)CTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCCAAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAG(A/G)GCTGCCCATGTGCCCTGTCTTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAAACACCATGTCCCTAAAATGT(C/G)ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTTCC(A/C)GTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGGCTTCAAGCACAGCCCTGCCCC(C/A/G)TCTTGA GATTTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTTAGGTCTTCTGTGACATTTCCCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCTT/CJTGGTTACACATCTT AGJACAGCAGAGCTGCCCTGAGGGAGGGTGTGTTTAAATGCTATGCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCTT/CJTGGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTGTGTTTAAATGCTATGCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A G A T A A A	GGGAGTGGGG	CGTCACCTGCG TTCCA	CTGTTGTGCTGAGAACAGAAAGGGGTCAAGGGAGTGGGGAGTAAAA(A/G)ATGGAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGTAGCAACAGAGGTAATG

WI-18064	54	G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCCTGTGGGTAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTCAC AATCATACCACCTGGGGAGAAAGAGTAAGCACAGTGCCTTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TTCCAGTTGGT	CCCTGGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATCTTGATCATGGGTGGAAATTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAG[T/C]AGCAGGTGCCGAGGTCTGGATCAGAAAAAAAGG CAGGCA
WI-18070	28	A C	AACCCACTAC TTACTCAGAGT	AAAACCTAATA AGAAACTGGA GGTTTT	AAACCCACTACTACTACAGAGTGTGTAT[AC]ATATTAAACACATGAAAGATAATACTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C T		---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG TTTGACTTTTAT[C/T]TCTTATGTAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	G A		---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCC[G/ A]TGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63	G A		---	GTGGGCATCCTATAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGGTGTGAA
WI-18115b	71	C T		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTACCTTTGGTATCC TTC[C/T]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70	C T	TTAGTGTAACCT TTGGTATCCC TT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTACCTTTGGTATCC TT[C/T]CTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAGAAAGGGGTGAG TCAGT
WI-18136	78	A G		---	TTTTGAGAAGCACTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTA GGTAATTTGC[G/A]GTAAGAACAAATAAAGCAATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115	A G	CCATCTTTCCG	GAGTTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTCAGGAGGAAGGTGTTATCCAGCAGCCATCTTCCGGAAGCTC[G/A]GTGGAGCACAAGCAGA ACTCGGTGGTAGAGTGGGA
WI-18190b	26	G A		---	TGAAAGAAGTCGACACAGCGGACACT[G/A]TCATAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGACAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62	A	---	---	---	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGAACAAAGGATGAAGCTAATCATGGAG[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A	C	CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACACAAATACAAACAAACATTAGGAACAAAGAAATGTGTAATCCAA TGTGTGAAAAATATATACAAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTGTTCTTGAAAC
WI-18215	78	A	CTGCCCTC	AGCAGAGTTC	OCTCCCTCTCT OCCC	ATTCATAGAAGCAATTCCTGAGTACAACTAGGGGACAGGTATTTACAAAAACAAATAGAGCAGA GTTCCCTGCCCTC[G/A]GTGTGCGGGGAGAGAGGGGATTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60	T	A	AA	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/A]GAA CCCTGAAAAACCTTTATTTGAAATTTGAAGTTTTCCTCAGAAACTGGCAGAACTTTTCACATTCTG AC
WI-17892	76	T	C	ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATAT[C/C]TGTCTCAGTAGTCTATTCACCTCTGTGGGCATTTGGCAGAAAGTGGC
WI-18242	30	G	A	AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACTG[A/G]AAAGCTGTACAGTAGAAGTGTAGCAAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C	T	---	---	GCATCAGACATCACCACCTCTGAAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T	C	---	---	GCATCAGACATCACCACCTCTGAAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[C/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C	T	TTCAAA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACCTCTGAAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A	G	AA	GGAGAAAAAGG GAGCAGAAGA	CTGAGCCCTCTGGATATGTGGTTTAGTGTCTATCATTAAATTTGGAAAGCTGCAGCTATTGTTATTTTC AAAT[A/G]TATCTCTGCTCCCTTTCTCCTTTTCTGGGATTCCTATCTGCAATGTGTTATA
WI-18330b	66	A	G	---	---	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGAATAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTTGTGAT TCACA

WI-18330a	49	GAAGA	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAG[G/A]CTGAGGAACAAGA GGGATATGTAGGCGAGTGAGTCAGGACTATGCAAAACCATAAAATAAGAACATAATTTTTTTGTTGAT TCACA
EST37564 5	85	TCAAGA	AAATTCAAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATTCJCTCATTGAGGCCCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	GAATT	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAAGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATCGGAGGCAGA GT
EST37624 6b	102	GA---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGACGCTGATGG CCTGCAGTCTCTGCCGTGCTCTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCCGTCC TCTGACCTCCCATTC
EST37624 6a	58	CT---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGAC[G/C]TJGCTGA TGGCTGCAGTCTCTGCCGTGCTCTGGCTCTCTGGACGTTTCATTCTACATGGCTGCTGCTTTGCCGTCC TCTGACCTCCCATTC
WI-18357	89	CGCATCAA	CCCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTGTGAGGTGGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAAC[G/C]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	AG---		---	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	GA---		---	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CTCCCT	GCCACTTTTGC CCCT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTTGAAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
WI-18012b	46	TC---		---	
EST38390 4	75	AGCTGCAATG	GCAAAAAGGA GCTGCAATG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGTA[G/A]TTAAGTTTATTAAATCAGCTGACTTTAGCATTGGAGATTATTCTGGAT

EST38512 7	91 T	TAATAAACTGACCCAAATGGTAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTCGT/GJGCTTCCAGAGTGCAGTGATAACTGTTATAGCC	CACTGCACTCT GGGAAGC	TGACGATGCC GAATACTTCG	TAATAAACTGACCCAAATGGTAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTCGT/GJGCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACCTCCTAAAAGATCTTTTC/TJCCCCCAAGTCTCAACAGAATGGTATATCTCTCTGGA AGATGAACGTCATCAATGGATTGTGCTGCTCTGTTTCAGCTTTGATTTTTTTTGCTTGAGAACCTTG TCTGTTAGGAC TTGGGGA	TCTGTTAGGAC TTGGGGA	CCTGCACCTCCT TAAAAGATCT	CCTGCACCTCCTAAAAGATCTTTTC/TJCCCCCAAGTCTCAACAGAATGGTATATCTCTCTGGA AGATGAACGTCATCAATGGATTGTGCTGCTCTGTTTCAGCTTTGATTTTTTTTGCTTGAGAACCTTG TCTGTTAGGAC TTGGGGA
EST38575 1	66 T C A A	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTCTGTTTAA T/CJCTCTTATGTGTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA	AGGGAAGGTA GTATAACACAT AAGAGA	GAACATCCCA TGTTTCTGTTT	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTCTGTTTAA T/CJCTCTTATGTGTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCATCTAGGAGGCTACCTAGCTCTCTGTGCTCCAGAGTGGTGCTCAGCCCGGGGCCCCGCTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTTC/GJGCCAOCATCCATTCCTCCAGGGG	GAGGAATGGAT GGTGGC	CCTGCTCCGCC CTTC	CCATCTAGGAGGCTACCTAGCTCTCTGTGCTCCAGAGTGGTGCTCAGCCCGGGGCCCCGCTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTTC/GJGCCAOCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TATAGTAGGTACTTTCTGCTGTCAGCAGGAATTTATTCAGTCTGAACCTGGGCAATTTCAA/TJGCGTG GTATTTTTTCTCTTTCATTTTTTGCAAGTAAAAAATCAT	TTGCAAAAATG AAAGGAAAAA	TCTGAACTGGG C A T T T C A A	TATAGTAGGTACTTTCTGCTGTCAGCAGGAATTTATTCAGTCTGAACCTGGGCAATTTCAA/TJGCGTG GTATTTTTTCTCTTTCATTTTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T A C A	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA/TJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGAGAGTTAAGATTTGGACCCAGGAGTTGGTTCCAGCATATA GGATCCTCACTACCTGGAGAGCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCTTJAGJAGGCCAGCGGGATGTGTGCCCTCCTCCTCCCAACTCATCTTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA	CAGTGATGGTC CTTAATCTTCT ATC	AATGGTCAATTT TAATATATCA G T T T A C A	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA/TJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGAGAGTTAAGATTTGGACCCAGGAGTTGGTTCCAGCATATA GGATCCTCACTACCTGGAGAGCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCTTJAGJAGGCCAGCGGGATGTGTGCCCTCCTCCTCCCAACTCATCTTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
EST38707 9	75 A G ...	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG/GJCCCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCACC	TCACCATCGTG GACTTAAGG	TGCTCCCTGA GGTGATATGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG/GJCCCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCACC
EST38759 2	86 A G G G T A T A T G G	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACAATGGTGG	GGCTTTGCTCT GAATTCAAA	AATCAATAGG AGAGGATTGG	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACAATGGTGG
EST38775 1	40 T A C	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTTAIGTGTGTTTCATTCACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA	GCTGACTGGCA CATGCTTT	TGTTTATGAGA ACCCATTACA C A C A	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTTAIGTGTGTTTCATTCACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38815 4	91 C A C A	TCCTTACTGTGCTTACAACCTTCTCTCCAAAGTTTGGGTGGTTCCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAAAGAAACTCATGAC/CJTTCTCCTTGGACTCGCTCCTCTCCCCAATCTCGAT ACCGACTGCACTGTTG	GGAGCGAGTCC AAGGAGAA	CACGAGTAAA AAGAAACTCA T G A C	TCCTTACTGTGCTTACAACCTTCTCTCCAAAGTTTGGGTGGTTCCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAAAGAAACTCATGAC/CJTTCTCCTTGGACTCGCTCCTCTCCCCAATCTCGAT ACCGACTGCACTGTTG
EST38858 4	98 C T T G A C	CCCTTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGTCG ATGCT/CJCTGTGTCCTCCGTCCTTCCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA	GGAAGGACGG AGGACACAG	GCTGTAGAATT TGTCGATGC	CCCTTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGTCG ATGCT/CJCTGTGTCCTCCGTCCTTCCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA
EST38865 2	72 T C T G T G C A T G C				

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAACATCAITTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCCC TTATTCAATGTCATCTCACACATCTTTATTTTATTTGTTTTCACATTTCTCAAATATCGGATTGTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCA/CJGCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TTATTCAATGTCATCTCACACATCTTTATTTTAT/CJTTGTTTTCACATTTCTCAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTTAT TTTT	CGATATTGAG AAAGTGAAAA CAA	
EST38909 5	47 A G	GCACAGCATG GCTAAAAAG T	GGTATTGTTG ATTCCCATCTT T	GCACTAACTAACTTTCAITTTGTGGATTGCACAGCATGGCTAAAAACG/CJTAAGATGGGAATCAA CAAATACCATTAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACACACTACACATCAAAACCTTAGGGAAATGTGGTTAGTGTGTACGTTGAG GGAAACTTATAACCTCAC/CJCGCTTGTTCACAAAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACTGCAATCT CACCCC	TAAACATCCCATTTGAATCCCTTGTGGG/CJGGGGGGGGTGAGATTGCAGTGTCAAGATAAA TATCACAATATATCAAAAACCTTCAAATTTGTCTATGCATTACACACTGACATGAGCCACAAACATT CCTTTCACAGGACTGTAC
EST39002 0	42 G A	GGACCCCTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGAGATCCGGACCTTCGGTGAC/CJAGGGCTCCCTGCCAGGGCTTGG CCCCTGACCCGGGCTCCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG GAGC	CACGTGGCCCTAAGTTCCGGGTCTTCTCAGTCTGGATGGCTGTGTGGAAGAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGGCAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTCAITCACAACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCCTAAAAT CCCTATTATTCCATGATATTTTCA/CJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTTGCTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCATTTTCTATCAGGTTTCTGGTCTTGTCTCTCAATTTTAAACATT T/CJCTTTTATATAGGGAATAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCTCCAGTT
WI-16406	24 C T	GCTTTAATGGC TACAGAAAGA AGG	CCAGAACCCAG ATGTGTTTAA AA	GCTTTAATGGCTACAGAAAGAGG/CJGGGTTTATTTTCTTTTTTAAACACATCTGGTCTGGCAGC AAGTTATATTGCAITTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAAGTTCCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGATTTGTTTCATCTGAGAAATAAACCTTCCTGTCTAAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATAATATTACCTGGCAATGAATGAGGTGTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTTACCCCAAGGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C		---	AGAAAACATTCTGTCTGATCAGAGGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAGAAAATGTTTGATATAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG TT	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAATTTCCAGTTGAGCAATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAAATCAAAATGCTTCTCTTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G		---	ACAAAGTGACATATCCAAACCAAC[A/G]TCCATCCCCACCTGTGCCCTATTCTTCTTGTGTTCTTT AGAGCCTTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCCCTCCCCGTACTCTCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTITGATT	GGTCCCTTATG AAGCCACC	AGGTTCTCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCCTGCATT TTCTGGGTGGGCCCTAGGTAATTTCTGTGCTCTTTGGTCCACAGACACAATTTAAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAAGTATGTT[C/A/C]CAATACCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCCAAGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTTGGAAAGAAAATAACAGGAACCTATTTATAT ACGTAATACACTTTTATACCTGCTTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAATAAATAACATAAACGAACGAACAGAAA TGACAGGAGGTGG[C/A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTCT GTAGACATCT	CACATTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTGAAGTTCAAGTCAAAACCAATTC
WI- 18387b	84 A C		---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTTGGTGAACCCCATACATTTTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGCTTTGTGAAAAGTGTAAATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC[AG]TTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGGAACTT GAAACAC	TTCTTGGGA AAGGGTC	TCCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACAC[AG]GACGCTTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT AGGT	GCACACCTTC ACACTGTTA	TCCATTCAAGTATCACATCTTCAGGATAGGT[AG]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGG CA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTTCTGGTCTTTATTTTGGACA[CT]GTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATAATTTTCAAAATTTCTCATCACTGTAAATCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATCTCAGC ATTGCTATAAG C	AGAGACACAACAAGAAGTAATAGGGGAAATGGGAAGAACAGAGTGAATTAAGCAAAATCTTGA TTCAGATTCATTAAACAGGAAGTTCTCAAAAAAAATCAAA[CT]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAATTTTAC TC	AGAGAGACAACAAGAAGTAATAGGGGAAATGGGAAGAA[CT]AGAGTGAATTAAGCAAAATCTT GGATTCAAGATTCATTAAACAGGAAGTTCTCAAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATTC A	--- OCTCTGTTGT TGTTGCA	AGCTGATCAGCTGTGCTTACTGTGTTTATGTGGCCAGGGAAGCCAAAGATCAGACACCTGTG CTAGACAGATTCA[CT]GCACACAACAACAGGAGGTGGGGTCAACACGGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CTTTTGGCTCT AAGTGGGACT A	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCGGGTGGAACATAAAAGGAAAGGAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCCAGTTCTTTTGGCTTAAGTGGGACTA[CT]TTC TGATACAGTCAGGGGAG
WI-18449	129 C T	---	---	ATCGCTTCAATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCCTGATGCTGTGTTTGTGCACATTGGGGCCACAG[CT]AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18457	120 T C	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTCT	GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGA[AG]TAGAAACCATCTCAAGCCTAAAA TATTTACCATACATCCCCCTCACAGCAAAAGTTTCTAATCTCGGTTTAGGACTCCATTGAG
WI-18462	39 A G	GGTGGGGTGC	GCACGATGGGA GTGACC	TGAGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGTGCAGAG[CT]GGT CACTCCCATCGTGCCCTGGCCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	G A	AACAAATGGT AGGTGGTATT		CGTGTGCATTT TCITGTAATCC	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCCTAAAACACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAACTATTATTATAATCCAGAATGAC[G/A]GGATTACAAGAAAAATGCACA OGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT		ACCCTTCACCC GCCC	AGCCCCCTCAGTCCACTCTGCTTCCACAAAGTCGGCTCCCAGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGACGGGCC[CT]GGCGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTGG ATGGTGACTT		GGGGAOCCACC CAGG	GATCTTGAAAGCAGCTAGAAACTAAACATCTTACCAGGTGCTGAAGAAAAGTGCTCTCGTTTTTAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTT[T/C]CCTGGGTGGTCCCCCATAGATTCAACCAT TGCCCTAATGGTGICTA
WI-16543	67	G T	AGATAAAC-TA CATTTGGGTTT		GATTCATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAATCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG[G/T]AAGTCCCTGTAAATGAATCAAGAAATCCTCAAGTCTGCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGAA		TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAACCATCTCCCCCTGACCCCCAGTCCATGGAAAAAATTGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTACAAAAAGTAATT G
WI-17690b	79	A G	---		---	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTTCTAGCTGTGTTGATTT GGCTCCCTAT[A/G]GATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTTT		CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTTCTAGCTGTGTTT[G/A] TTGGCTCCCTATAGATTAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT		TTGAGGCAATA ATCCAGCTC	GATCCAATCTAGTGTCACTCACTATCCAGATTATTC[TT]GAAGTGAAACCCACCCCTCCGACCC TGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAAGCTGTT[C/T]GAG CTGGATTATTGCCTCAA
EST51717 a	39	C T	---		---	GATCCAATCTCAGTGTCACTCACTATCCAGATTATTC[TT]GAAGTGAAACCCACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAAGCTGTTCCGAG CTGGATTATTGCCTCAA
EST53012	97	C T	TGGTCACTTG GGGC		GGCTCTGOCCA CGCC	TTTCCAGGTTGACAGGTTTTATCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCQ[C/T]GGCGTGGGAGAGCCCACTGGGTTTACATTCCTGT GGGCAGGTTGGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCAACAATG TAC		CATCTGGATAT CTTGTCAACATT TT	AAACTGCAATAACAAAAACAAACAGAAAGTCCAAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAATGTGACAAAGATATCCAGATGTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAA CA		GCCTTTCTAA CAATAAATGCT C	TTTCCAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGCTTACACTCAAATAGGTTTTAACATGAAC ACATTAAGGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117 C G ---			ACAAAGTTCAAAGGAGAACCTCCCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCCTAGGA AACCATCTGGGTTAGCCCATAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A			GCTTGCTTTTATGTTAGGTCGGGGGAAAGGAAGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGAGGTTTGCAGAACTCTTTGCTTGGCTAACAGTCTGTATGTGACAAATAGCCA AACCTCCTCATTCCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGAAAGTAAACCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT[C/G]AAATAGAAAACTTATAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGAAAGTAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACTTATAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C GGCACTCTCT			CCTACAATCCTATAATTTCAAGGGTTGGGAAGGATGCAGGAAACAGGCACTTCTTAT[C/G]GCC TTTGTGGGAAGGATCAATTTGGTGCATGCACCTTAGGGGACAATTTGGGAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125 A G ---			TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAATTATCCAGAATAATTTCTATTGAATTGA CTGATTACAAAAATGTTAACAGCTGGATAAACCGTAAACGATATGATTCATTCACATGA[G/A]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC			CCAGGCTATAATGTTGGTGGTGGATCT[C/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTG TATTTTITAGTAGAGACATTTGATTTTTAGTAGAGACAGG
TIGR- A004X20	25 T C GA			TAAGTTTTCCTTCTCTCTGTAGGA[C/G]GTCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACCTCTGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGTTACCTTTGTTCTGTGTCTTTCA GACCAACCGCTCTCTTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTGCTCT
TIGR- A004X30	26 T C CCAC			TTTTGAAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACTTGTAAATAAAATTAATAATAGTTTT AAACACTTCCATAAAGAAATTAGGGTGGCCAGCTCCTTGATTTCCTCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT			CACGGTATATGCCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACCTT[G/T]GCTTTCATGAAATTTCTAATTATAAGG ACTGTGCTTCTTCATATTCATTTCAATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTAAAGACTG

TGR- A004Z19	85 C	GAGAACAACT GCAGCAATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAAGTTTATTGGAGGAGCTTGACACCCCTCTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTTTCTCCGATGACCATCTTTGGGCTGGCGGCCAGGCGCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGTATAGGAACAGATC
TGR- A004Z42c	89 C	TTGGGGAGGT AGGAGACT	CAGGGCTGCG GTCC	GTCTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGCCAGGTAGCCTTCAGGGGCGGGCA GGTTGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTTT CATCATCTGTGCTTC
TGR- A005D17 c	81 T	---	---	TATGGACTGTGTAGAAATATGATTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTGCTAGATTCTCTGGCCTCTCTGCGAGGATCCCTCTCTGGGCAC GGGTGGGACCCCTCTGGAATGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TGR- A005D17 b	79 G	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTGCTAGATTCTCTGGCCTCTCTGCGAGGATCCCTCTCTGGGCAC GGGTGGGACCCCTCTGGAATGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TGR- A005D44	97 G	TTAACATTATT GAACTTAAAA CTGTTACAC	TTGTCTATTAT TTAAGGCCAAC AAAA	CATCAGTAACATATACACAATTTGGTCACTCAACTTTGCCCTCCAATATATTTCTATACAATACATT AACATTATTGAACCTTAAACCTGTTACACTGTTTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTCTTTGTTAC
TGR- A005E31b	27 G	---	---	GGAGTTCAAATTTATAACAGGCCCTG/GJCTACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCCTGCTTGGCCCTACAAAGCCACCTCTAT TTCATACCAATACCTTCTATTTTCATACCAATAAG
TGR- A005E39	182 G	---	---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAAATAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGAAATGACCCCTTGGGCTCCTTTATTTGTTCTTTTCAACAGGACC CCACAGATATTTGCGGTATGTCATGAGGACTGGGGATGCTTCTATTG/GC/GGATGCTTCTATTTT
TGR- A005E42a	42 A	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAG/GJCTCAATTTCCCTGATTTAGGA AGCGATGCTAATGGGTATTGCATAGGTAGTAAATGTTGATTTAAGAGAATCCCAAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAAATAATAG
TGR- A005E46	76 A	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCTACCCGTTTGTAAAGCACCTACTCGGTATCAGGCACCTGACTCGG TGCTTTAC/GJTTACATTACCTCACAGCCAGGGTTGGCAATGGTCAITTTTGACAAATGGTCAITTTG ACAC
U20979	24 C	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/GJGCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGCTTACGGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCTTTGATATTGTAAAAATTTCCCCCAAGAGCCGCATATGAAATCTGCC

X57830	106 G C T	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTCGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGATCATATCTG/CJATGCCTCATTTTATTTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCAATTCAGCTGTGAG CTTTC
X74070b	72 T G TGGATC	CTTTTAAGAA ATTTTGTITA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCT/GJGATAAAATCTAGATCTCTAATAATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTT CAGTTTTCCTTATACACAATTCATTCTTTCAGCTAATTAAGCCGAAGAGCCTGGGAATCAAGTTT GAA
Z48804	44 C T ---		---	ACTGCCGAAGTGTAGCGGCCCCCAAACTTGCTCTCATCACCAG/CJTJTAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACAGTGTGAGAAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133 A G ---		---	ATGACCAAAGCCACCACATTTAGAACTTTGGCTGCCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCOCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGC/JA GJTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA/JGJTCTCCAAGTATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACTACTGCTTCTGTCTAC
D29833a	21 A G ---		---	CCACTCCATCCTGATGCCCA/JGJTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCCTCAAGTATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACTACTGCTTCTGTCTAC
D31762	82 G A ---		---	CTCCCTGCCTCCTCCTCCTGCTGCTGATGCTCCGCTCTCAACACAGCCGAAACCTGCTTGCAATGGGG GAGGGGGGCTT[G/A]CTTTCTCTCTCTGCTTCTGCTTCTCTTATCTTCCACAAACCACTTCTCAATAAA GCCAAAATCTTCTCTCTTCTCCCTCAGGCCACCTCCTGTCTCCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64 T C ---		---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG[C] CCCAGGCTCTGTCTCCTCAGCTCATTTCTCTACTCTTTTCTCTATATACTCATCTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101	C T	---				CAGGCAGGACTTCAGTGTACGTATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTATTTTCCCTGTTCCAC/C/TJGAAGAGGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTGTCTCCCTCCCGCTCGGCTTCJCGGTGCTGGAGGGTGACCTGTCCACAGATGAC
D90145	21	T C	---				TGGGAACATGCGTGTGACCTC/CJACAGCTACCTCTCTATGGACTGGTTATGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTAAATTTAAATTTATATACTATTTAGTTTTTATAATTTATTTTGTAT TTCACAGTGTGTTGTGATTTGTCTGTGAGAGTTCCTCCCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T C	---				ATTATCACTCTCAAAAATTTTGGTGTGTGTTTAAAGTACTTCTTATTTATGAGCCCCQ/CJGAGGA CCAGACATGTTATTATCAAGCCCCCTATATACCATCTAAT
EST16668 5	71	C T	---				GCATTTTAAATTCACATTGAATCATTTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TJGTAGATTTTCAGATGTAGGTGTCGTCATACTGAGCACCTTATCT
EST16904 7	57	C T	---				ACAGACTATCGCCAACTTATAATGCTTAAACTTTATGATCAATAGTAATAAATTTACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	49	A G	---				TTTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACGTGATACACC/CJG/TTACTACTTACTC TTCACCTCTTCAAACTGATTCCTTAAGACTTCTACTTAGCAAA
EST21885 6	80	G A	---				GGCTGTAAGTAGAATCAAGGTTAAGAACAATTTATGCACCTTATCCACAAACATTTTACTGAGCATA CTAGGTGCTGGG/CJGTGTGACAGTGTGAGCAAAAACACAA
EST22623 8a	26	A G	---				ATTTTAGTGCAAAATGACAAAGCCCA/CJGAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644 2	98	A G	---				AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/CJG/AAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31	T A	---				CCTCATTTATTTAAAAAGACGGACATAAAAAT/TJATATACAACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106	T C	---				AAAGATCTGGCATTATTCACATCATTTCTAAATATTTGTAAATACTTTTCCATGAGTATTTTTTCA TGTCACAGCATTTTAACTATCATTTAGCGTAAATACC/CJG/AAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAATT
EST24308 3	45	A G	---				TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/CJG/CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73	G A	---				CTTGAACCTCTGGTCAAGTGGTACGTCGGTCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/CJG/JTGCCTGACCCACATTTCTTTATCCGATCTGTGTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T C	---				TATTGTGCATTATCAAAATGGTTAT/CJAGTTTTCAATTAACACTGTAATGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGTTAGTTAATGCTACATT

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EST25476 9	33 G A ---	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTTCTCCTCCTCTAAAAACCAACACACA AGAGGCTCTCTTGCTGCTTTTCCATGGACTGTGGCGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---	---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG ATT/AJACATTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	---	AGAAATAAGGTGCTACCGAAGCTCATGT/C]GATAGCGCTTTCTTTAGGCACATATTATAGCAAT CAGATGAAAGTTCTGTAACTACACACACACTGTGCCTTAACAACAACACCGTGACTCTGA
EST27816 5a	26 T C ---	---	---	CAACTCAAGGTACAAAGACAATTGCATT/C]TAACATTGTTATAATAAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATAACTCCATGTT
EST28588 0	78 A T ---	---	---	GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTCTGGGAGGCTCAGGAA ACTTACAATCAJ/V]GGTAGAAGGCCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 A C ---	---	---	TACTCACACCGACATACATATCTCAJ/C]GTAGAATTAGCTATAGCTACTGCATACTTAATTCTATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---	---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGJ/C]JAGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCTCTATGAATACTGGCAGCTGTTTATTTATGTTTATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	---	TGCTTTGTTCCCTCCAAATCCATAAAAT/C]GTGTGCTCTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTAACCATATTCAGTATTTCTGAATACAGGTTTCAGATAACTATGGAGATGATACCAT GGACTAGGTA
EST33352 7b	75 C G ---	---	---	TACACATTATCAAGAGACCCTGACATGCTCCTCCGCGAGAATACATTCGTCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATATTTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	---	ATTTTCCCACAGCAGAAGTATATTTATGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTCAAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAACJ/A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 A G ---	---	---	CCTTTGGGGGAGTTTAAAGCAGAATGTACAAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCAACATCGTCTATAGJ/V]ACCATTTCCTCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTAAAT AACATCAACTCAAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAAACATGCTATTTGAACAAACCTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGGTTTGAAGAAATATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA[C/T]CTTTGAACACAGCCTGAATCCCC
EST34739 3	97 T A ---			GAAGTATCCTTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[A/G]GTGGCTTACAACCTCAACTGACGAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAAGCTCTTTGTAAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GATTCAGGAATTTCTTAGTCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGCTTCTGGT[G/G]GGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]TGTCTTCTGGTGGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCACCTTACCTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCCTTCAAATTTTGTAGTAGGCATTTAATG[C/T]TATAAAATTTCCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACTTTTAGGCAATGGAA[C/T]TAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTCCCTCTCTGAGGTGGCACCTTTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAAAGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATTAACCTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTCAATGGAGA AGTTCCCTCCCATGAACCAAGA[C/A]CTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAAGGCTGTGA
EST36301 4	93 C T ---			CACCTGTTCAATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTTACCAAGTGTGCTCAGCCTACAGC AGTCAGGAGGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAA
EST36519 0a	33 G T ---			GCCATAGCCCAACAAAGACATGACTACCAACGC[G/T]GGCCCTTGCACCCATACTGGCCTCAGCAG CTAAGACTGGACAACCTTTGTACCTAATGACCGCCACCTGGCATATACTGGCTGGGCTCTTCTCTGT CACAGGGGCTTAGTCGT

EST36620 6	50 GA ---	---	GAC TTATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTAAATATGGGAAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 CG ---	---	CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCTC[A/C/G]AGGGGACATATCACACATATTCTAAGTCACCTGTGTGACTCGG CTTGAGCAAGTCAITTTCA
EST36729 9	62 CT ---	---	GAGACAGAAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 AT ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATT[A/T]CTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 CG ---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGTATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 TC ---	---	GGTCTCACTCTCTTGGCCAGGACGGTTTGAACCTCCTGAGCTCAAGTGACCCCTCCCACCTTGGCTTCC GAAAGTGTAGGATTACAGG[T/C/G]TGAGCCACCACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 TG ---	---	AATAGTCTATGGCTACGGGCCCCGTGGGATGTTAAAAATGGGATTTTAAATTAGATTGTGAACATG CAAAACCCAGCAATTTCTCAGCTTATATTTTGAAGTCT[T/G]CAGGAGAAAAATGGGGTCC
EST37284 2	93 GT ---	---	AAAAACCTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 AG ---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCCTGCTCAGCCTCCCAGGTAGT TGGAACCTATAGTAGGAGTATC[T/A/G]CCCTGCCCTGCTAGAACTTCAAGTTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 CT ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTAGTTGAATATTCCTTCACATAGCCCAACACATTTTTTCAAGGCACCTCTAGCTACTACA GGA
EST37376 8b	101 GC ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAG[T/C]TGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTGTCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 TC ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAG[T/C]TGAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

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EST37378 9	63	T G	---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46	G A	---		---	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34	A G	---		---	CTAGGCATGGGGCTTTACAGTCAATTTATTTACC[G/G]GTCATGAATTCATTAAAAACCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---		---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACCTA[T/G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57	C T	---		---	TCTACCAGGTCAACAAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACCTA[C/T]CGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACCTCTCTCTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100	T C	---		---	TAAATCAAGGCCCTCTTTCATTACCAAAACAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTATCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25	T C	---		---	TTTATTTGCAAAAGTAAGCAGCCGGT[C/T]GGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGACAGCCCA
EST39053 6	90	T C	---		---	TTTTTTGTTACTCTGTAGCCAGTCAATATCTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[T/C]AAACAAAGTTACTGAATATTTTTCACCTCGTGGAGTTG
EST39331 1	70	G C	---		---	TCCTTCTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG[C/G]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---		---	GTCAACATTGACCTTACATAGTCCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T C	---		---	TTCTAATAGCATGCCCTGTGACAGGGGAACTAAGCTC[T/C]TCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42	A G	---		---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[G/G]ATAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACCTTTGAACCTAGTCCCTGCAAAAGCACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81	A C	---		---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCACTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGAATTTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68	A G	---		---	TTGATGGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTAAAGCT

EST51340	51 GA ---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATGAAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 TC ---	---	CATGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTCGAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTTCCTTGGTCTCCAGTGGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAAGT AGCTG
K01506	63 TC ---	---	CTGAACCTCAGCTGCCCTACAACTCCATCTCAGCTTTCTCTCAGCTTCATGTGAAAACTAQT/CJC CAGTGGCTGACTGAATTTGCTGACCTTCAAGCTCTGCTTATCCATTACCTCAAGCAGTCAATCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTG ATTGAGCCTTTTATCCT
L18877	69 TC ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGCCAGTGCACCTTCCAAGGCC CT/CJATCCATTAGTTCCACTGCCCTCGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 TC ---	---	GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTTGCTCGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCTAGAAAGAAAGGCTTTGGCCCTGGTGGTGGCATAGGCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTGAGACAAACCTGGGCAAT GT
L38517	137 GC ---	---	GGGTCCAGAAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGACCTGAGCTGGGGACACTGGC TCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCAAGCTCCCCAC CC[G/C]GTGCTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 TG ---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAAATACAGTAGTATTTCTTTTGATTTGTATATTT/GJGCGCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCCGTTGGCCCTGTGTTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 GA ---	---	CAAAGTTGTCCTCGCCCATGAGCACCAAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCAGACCAACAAATCTGAAC[G/A]TGCCTCTCCCTTCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	AAGTGAACAGAAAGCATGGATTGTTCTCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTGGTTTACTTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	GGCGACAGTCCAAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTTATTTCAACC CCATCAAGTATAAGGTTACTGATTGATGGTCCTTTTATAAACATTGGTATATTCCATTCATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	TAGGATCTGTGCCAGGCCATTGCGACAGCCACCCACTCCACCCCTGTAGTGTCTCCACCCC TGGACTGGTGGCCCCACCTGGGGAGGCTCCCCATGTGCTGT[C/G]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGAGGGGCTCCGCCCTCCCTCTCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCATCCAGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT[G/G]TTTCTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTTGGGTC
M26041c	173 A G ---	---	CTAGCATTAATTTCTGGCCCCATTTATCATATCCCTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTTCTCAAGTGTACCTACTAAG[G/G]GATGCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M26041b	157 A G ---	---	CTAGCATTAATTTCTGGCCCCATTTATCATATCCCTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTTCTCTCA[G/G]GTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M26041a	45 C G ---	---	CTAGCATTAATTTCTGGCCCCATTTATCATATCCCTTTCTCCTCCAAATGTTTCTCCTCTCACCT TCTCTGTTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGAC TTCTGATTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M63967	57 G C ---	---	TAAGGAGCTGTGAGGGAGGCCAGTCACAGTCCAGCAATTCACACACCCTTGAC[G/C]AATGCT TGCCAAAGCTGTTTTAAAGCCAAAGAACACCCCTTTCTTTGTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATCAATC
M81695	34 G A ---	---	ACTTACTTACCCTCACCTGTGAGGCTGACGGGA[G/A]GAACCACTGCACACCCAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTGTCTGGGAGGGGCTTTGTCTGTCAAGGTTTC CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACG T

U06641d	166	C T ---	---	CTCCTCCTTTATTTAGCATGGAGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAACATCTTTC ACAACTTACCTTGTAAAGACAATTTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAAATT TATTTCCAGGCTATTTAATACGTACTTTAG[C]/TGGAAATTATCTATGTCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39	T C ---	---	GAGGCTTATGAGGGTCTCTACTTCAGGAACACCCCAIT/C/GACATTGCATTTGGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTCTGGCCCAAGGAAGCAAGCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---	---	GAGCAGAAGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C]/ACATCTGCCCGCCCTTCCAGCCCTTCCCCAGCCCCCTCTTGTCTTCTC ATTCATTCAACAAAATTTGGC
U10694	20	C G ---	---	GTGACATGAGGCCCATTTCT[C]/G/GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTCTGGGTTCTTGTCTATTTGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTTAAATGTCAGTTTAAATGAACCTTCAACATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---	---	AAAAGGACTCTGGTTCAAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGAGGATTAGTGAAGTTACATGT AAGCACAGAGGAACAGCCAAAGAGAT[C]/CTTACCGTGGTCTTACTAAAGTACATATCCTTAACTTGG GGTTACCTTCAGCA
U15555	187	T C ---	---	TTTCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCAATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C]/CTGGTCTCATAC CTCATATGCAGGATTTCATTCA
U17077	122	T C ---	---	TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTACAGAAACGTCCTTGACAGCTGAGCGATGACACCACACT[C]/TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGGGAAAACAACACTGTCTCTTGG AATTA
U18543	58	T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCAGCTGGGTAGTTCTAGAACCTT[C]/JAGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCCCCTCCCGGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACCTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGAGCC

U25975b	164 C A ---	---	---	TCAC TGTGTGGCCTACTCTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAATATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAC/C/AAGATGACTTTTATATGAACCCCTTCTTTAGG GTCAGAGGAATGTGGACTGA
U25975a	143 C G ---	---	---	TCAC TGTGTGGCCTACTCTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAATATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAAC/C/GAAGAGAAAATTGCAAAAAGACAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCAGAGGAATGTGGACTGA
U25997	61 A G ---	---	---	CAGGAGAGGTTATTCACAACCTCACCAACTAGTATCATTTAGGGGTGTGACACACCA/C/GJTT TTGAGTGTACTGTGCCGTGGTTGATTTTAAAGTAGTTCCTATTCTATCCCCCTTAAAGAAAAT GCATGAAACTAGGCTTCTGTAAATCAATATCCCAACATTCTGCAATGGCAGCATTCGCCAACAAAA TOC
U28413	29 C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTGTGTACCTCAGTT G
U30884c	89 A G ---	---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGT CTTCTATCCCACGTTAGCCA/C/GJTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAAATCTAT TGACGGAAGTCATTAGAAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCCACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGC/C/GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCACGTTAGCCAATGTCTTGATGAATCTATATGAGTCATAGAACACAAAATCTAT TGACGGAAGTCATTAGAAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCCACAGTTGAACACAAGT GCTGTCA
U31216b	78 A G ---	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTATCA/C/A/GJCCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCAACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGCGGATTTCGCTTAGCCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC/GA/JTCATCAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCAACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGCGGATTTCGCTTAGCCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ---				AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G]CCACAAATCTGGTGCTCTCTCTTGCTTACAAATGCTAGTCCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTCTACCTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---				AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]TTCTCACGCCACAAATCTGGTGCTCTCTCTTGCTTACAAATGCTAGTCCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTCTACCTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---				ACGGGTCAACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCAGATTGTCCTCC AGACCGCAGG[C]TTCCCCACAGCTCAGGTTGCTGGAGCTGTACATGACTGCCTGCCAGG GCTGCAAGCAAGGCTTGTCTTCTATCTGGGGACGCTGCTCGAGAGGCCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 A G ---				GACCAGCTGAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[AG]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAAATGCCTGGCCGAGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---				TGAAACCGTTTCAACATGGAATGATCTGATTGACTAAT[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTATTTCTCTCTAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACCTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---				TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTACTGGGTGTAA AACCACCTTGAGCCTCTCTGAGACCATGTGGTTTTAAAJATATCCATAAGGGAAGGTACCCACAG CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAAATTTGGATTCTCTGTTTTTCATGCTCTCTCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---				AGGAAGATCCCACCGACCTTCTCGCCTAATCCTTTAGATTAGGTCACATTACATTAAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAAAATTGCG AAATCTGTTGTGCA[C]TGCTCAAATGAAAACGCCCTTCGGCTTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCCT
X52011a	118 A C ---				AGGAAGATCCCACCGACCTTCTCGCCTAATCCTTTAGATTAGGTCACATTACATTAAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAJ[C]GTTGCGAAAAATT GCGAAATCTGTTGTGCACGCTCAATGAAAACGCCCTTTCGGCTTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTTCTCTCCAC/A/GJTGACAGCTTCCTGAGTCAGCCCTCTGTCCAGCCAGCTCGT GCACAAATGGAACCTCCCAGGGCTCCAGGACTCGGGCTTGCAGGCTTGCCAGGCTTGCAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTTGCCCTTGCTGCCAGCCACCTGGCCCCCTTCTCC
X54869	99 A G ---	---	AAGCATTTGCGTTACAGTGCATCAGATACATTTTATATTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTATGTTATTTGCTCT/A/GJATACAAAATCTAAATCAATATTATTGAAATAG GATGCACAAATTACTAAGTACAGACATCTAGCATTTGTGGGGCTCATTTGCTCAACATGGTA
X66924	147 G A ---	---	GCGTGTCTGCACCTCCAGAACGAGGTGCTGGGCGGCTTCTGCTGGGACCGCGGAAACCTCTC CTGCCGGAAGCCGACGAGGATGGGCGGCACTTGCGCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACT/G/AACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACACTTGATTGTATATAAGATAA/T/GJT CATACTGGAGAAAACCTCCAGAAGGTGACAAATGTGACAAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTTATACTTGAGAAAAATTGATAAAGAAATGGAAGATCA TTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTCAACCCATAACCTCAACCACATCT/GJATCTCCACCCACATCCCACCACATCCACCTCCATCC CCAAACCATCTCATCCCCAACTACAGCCCCAAACCCAGCCACAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80197b	99 G C ---	---	ACCCAACTCAAGTCCAGGCCCGCCAGGCATCTTCCTGGCTGCCCTGCTTGGCCCATCCAGTCCAGG CGCTGGAGGAAGTGCTCAGTACTTCTCTG/CJACITTTGAAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	ACCCAACTCAAGTCCAGGCCCGCCAGGC/A/GJCTTTCTGTCCTGCCCTGCTTGGCCCCATCCAGTCC AGGCGCTGGAGCAAGTGCTCAGTACTTCTCTGCACITTTGAAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACCACAAAGTCCAGGAGGGCGGCGCTCGCCGTGTCGGTGTCTTTCTTTT CAGCCCCGAGAGGTCCTGACCTGGGGCTTCTCCAGCCTCACTGCGCCACGCTCCCCGCCGCTCT CTTTCTCCCAGC/G/AJAAACCAATGCGCCCTTCACCTCGCGTGCCTGCGAGGCGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGCCCCCAGACGTGTCACAGGGGAACCTCTGCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGAAGATGGGGCTT/GJGGGC ATGCGCAGGAGGAGCCATCGGGTACTACGACGCAACACTCACTGTCCAGGCTGAGATAAATCC GGGA

X87344	34 C ---			CATCCAAAGGCACTGGTGGTACTCTGCTTCTCTGTC/TAAGTACCAAGAGCCCTCTGCCTGTGCACTGC AAGCTGTGCTACTCAGGCCCAAGGGGACTCTCTGTTTCCATTCTCCCCACAGACCTGTCAAGAG AAGCATGACAACAACAAATCATTACCGACTTTAGTGCITTTTT
X87838	179 GT ---			GGTGGCTGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAAACTTTTGTCTGGTCTTTTGGTCGAGGAGTAAACAATACAAATGGAATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAAGATGGAATTTA/GTCAAACCCCTAGCCTTGCTT GTTAAAAT
Z14138	81 A G ---			GTTCTGCTGCCTTACACAGGGGCCCTGTACAGTGAATGGTGCAATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[A/G]TGAATGTGCCCTCCAAGCGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAGGTCTCAAGGTTCTCAATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191 A C ---			TAATCCTCACCATTCTCAGGTATAAGTTCTATAAACAGGCTTGGGAATCTGGGTAATTAATAACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTACATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTCC CAGTACTGGTTTCCAA
Z23091	159 G A ---			AGAACTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGTCTGCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTTCTCTCTCTCTCACTGCGAGGCCCTCCCTTCCCTCCTCCTCCCTCCCTCCCG CTCTGTGCTCTTCAATCTCA[G/A]GGCCCGCAACCCCTCCTCTCTCTGTCCTCCCGCCCTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125 A G ---			GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAACCTGACCTAGTTGTCTCCAGGACCTA[G/G]CGGTGC TCACTACCTTGTCTTTGTGTTGAAGGAGTGTTTCCATGACTGTTTAAAGTGACAAGTGCCATGG ATATCTACACCGTACACAGACTAGATTGTCTCAATGTCCTTGCTTGGCTGGAC
11595	125 A G ---			GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAACCTGACCTAGTTGTCTCCAGGACCTA[G/G]CGGTGC TCACTACCTTGTCTTTGTGTTGAAGGAGTGTTTCCATGACTGTTTAAAGTGACAAGTGCCATGG ATATCTACACCGTACACAGACTAGATTGTCTCAATGTCCTTGCTTGGCTGGAC
1241	131 G T ---			TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTTATCCTAGGAAATAGAACACACTTTGAA TGGTCTTTGCTCTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCAGCTTGT JGCAGGAGTGTTTAGGATGAAGAGAGAAGATTAAAGGAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAAATAGGAGGCCCTGAGATCCACTGGATGTAATCTAATAAACCAGAGAGAAA

1282	130 C T ---	---	GTGCGATCACCACACAGTCTAAATTCAGATGTTTTCATTACCCCTAAAGAAATCTTGACCCATTA GCAATATTCCCTCATTCTGCCCTCACCCCCAGGCCCTACTCTTTATCGCTATAGATTGCC[C/TA]CT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTCTTTCACTGAGAATA ATGTTTCAAGGT
6810	68 C T ---	---	AGTACACACATACCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAACATTT A[C/T]AGAAGCATTTTAAATTTACAACACAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTG TTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGCTATGAACAAGTACAA TTTTCTTTTGAGTTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118 A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGTAAC[A/C]GTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGATCATCAAGATGTTGGACACCTTGTGTCAAATC TTGGTTCAGGTGGCGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C ---	---	CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G/T]TATACTATGACACCATTTGGGACA CAGATTATATATGTCAGACACCAACGAATGTCTTTAAGATATGACGAAGCACAATCTGTCTATGGT TTAACAAGAAATGAACGTCTAGG
6972b	149 G T ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAACTATTGATTATGCG CACAATTCAGAG[G/T]CCTGTTATTGGTCTATTCAGAGATTCACACTCTCTCTGGTTAGTCTTGGGA GAGTGATGTGTCAGGAAT
6972a	122 A G ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTCAGAGATTCACACTCTCTCTGGTTAGTCTTGGGA GAGTGATGTGTCAGGAAT

7598k	210 A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CAATGCAG[A/C]
7598j	208 A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CAATGC[A/T]GA
7598i	192 G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598g	142 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTG[A/G]GATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACAC[C/G]CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATT[A/G]GATTTACAAAAGACACCCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTCTCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGAGTCTATCTCTCAAGGTCCCAAT[A/T]CCTTGAGGTTCTCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTCTCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGAGTCTATCTCTCAAGGTCCCAAT[AACCTTGAGGTTCTCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTCTCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGAGTCTATCTCTCAAGGTCCCAAT[AACCTTGAGGTTCTCT
8071	119 A G ---	---	AAATACAGAAATTTATTTAGAAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCCAGGTGG AAAATGGGTCCCAATAAATGGAATTTTAGGGCAACAAAGTCTAAAGGCC[A/G]CAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAATTCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAAGT
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCATT TG[A/G]CGCAAAATCCACTTTGCTGTAAACGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAAGT
8498	84 C T ---	---	AGGGTTACAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTATGTC AACTGGCTTCAGCTAG[C/T]AATACCTTCAATTAATCGAAAGAAAAAATGCTTTAAGGAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCTCTCTCAATACAGAACCCAGGAATGTAATTTCTTAACCTCAG

WI-18562	29	G A	---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAAGTAG CTTCTTATTTCACATAGCTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCCTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C	---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCCTTCGATGCAAGTATAATTGTAAACCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T	---			TAAAGTGTTCAGGACTGGACT[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
						GACTTTGGTGATTTAAATGCTTTTCCCTTAAATATAGAAATAGGTGTAATTTCTCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAATACTACTACTGCCAACAAACACGGGCATCCACTCTGCTTCA TGCTCTCCGTGAGAC
WI-18520	75	G A	---			AAATAAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGACI[G/G]ACATGGTGGCTCACAAGCCAAAGATATT
WI-18563	94	A G	---			GTCCTATTTCAAATTTAGCTAGACCCATTTCAITCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC IT[A/G]GCCATAATTTAATCAAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18582b	69	T A	---			AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723f	94	G A	---			AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGTATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T C	---			AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A G	---			TTTATTACAATAATTTAGGTGGCACAAATAACTAACAGCTTCTGA[G/A]ACAGGAGGTAAACATTTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAAACTCGAAATA
WI-18619	44	G A	---			TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAAGGAGCCCTCCAGGTGGAAGGTAATTTTAAATAAAAAATAA TGGAGCTACAACCAACCCCG
WI-18715	76	G A	---			GTAATAAAGTTTTATTGGCACAGCCAGCTGTTTCAATCATATGCCATTGACATCTGCTGTGCCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGTCOCCCGTG
WI-18535	107	G A	---			AGAGTGGTCAGAACACAGCCGAATCCAGGCTCTATCACTACTAGTTTTCAAGTTCTGGCAGGTGAC TTCATCTCTTCGAACTTCAGTTTCTTCATAAGATGGAA[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAGATTAACTAATAGATGCATAGCACTTAAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGTCTACCAAGGCAGACGAAG
D17525	107	C T	---			

DWU-133c	313	A G ---	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAATAATTTGTTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAATAATTTGTTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAATAATTTGTTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTTGAGTTTGAATTTAATAGTAAC[CT ITCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---		ATGAGATCCTTTAAATCCTCCATGAACGTTTGTGGTGGCACCTCCTACGTCAAAACATGAAGTG TGTTTCCCTCAGTGATCTGGGAAGATTCTAC[CT]GACCAACAGTTCCCTCAGCTTCCATTTCGCC CCTCATTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGCTTTCTGAGGAG AAACAAATAAGACCATAAAGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---		GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACCTGCCAACAAAGTTCACTCATATATAAAGCATTTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAAATG[GT]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	--- --- ---	---		ATTTTAGTGCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTGTTAG GCCCTTCTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-447	85	A G ---	---		ATTTTAGTGCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA[AG]ATCACTGTAATTAATTAGTTTATTAGAGCACAAGCTTAGCTAAT CAACCATTTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTG TTAGGCCCTTTCTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-476	63	C G ---	---		GTAATAATTCAGTTTTTTCCAGTTCCCTCTTTTGTGCTGCTTCTCAATTAGCGTTTAAAGGTGAG[CT]AT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67	A T ---	---	---	TCATAAGGGCAGTATCTCCTCTAGCTAGTGGCCCATACAGAAAATCTATCACCATACAAAATTTA[A] A/TJTGCAATTTATGTTTAAAGCACAGGTGTACCGAAAACGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131	A G ---	---	---	AAATCCAGGGCATTCGAATCTGTTTTCATGATTTATAGAGGGTTACACAAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATCCAGATGTTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTTTTCCTTTCCTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGTCCTCAGAGTGAAGATGCCGAG
DWU-525	97	A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCAITCTTTTCAGCTTGTTCATCTATCTACTGTTGTA ATATACAGTTTTGTAAACCATATGATTGA[C/A]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTCTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAACTCTCTAAAATCTAGTCTCTGATTGC
DWU-59	94	C T ---	---	---	CATTCTTTGTGAAGGTAAATGGACTCACAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCGG CCCTTTCTTTGTGAAGTCAATGGC[C/T]GAGCCGCTGTTTCACTCCAGGTGGCAGACTCGTTTTCG GTAGTTTGTTTTAACTTCAAGGTGTTTACTCTGATAGCCGGTGAATTTCCCTCCTAGCAGACATG CCACACCGGTGAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C -- ---	---	---	CTTGATCATGGGGTGAATTTTGTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T ---	---	---	CACACTGGCATCTAGGCCTTCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTCGAGAA[C/T]G CTGGTTCCCGCAGCCCGCCACACCGGCTTTCACCCACACAGGCTGTGAGGCAGGAGGTGGTAAAGACGT AGCTGTAGACCCCAAGCAACCACCGCCCTGGGACCCCTCGGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAGT
WI-18014	40	A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97	T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACCTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTCATAA[A/T]A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT[C/J]AAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T ---	---	---	TGTAAGGTGACITCTATAAGCTTCTCTAAACTGTCAAACCTTTCATTTACTGAGATTTATTCAGGGCCAAT GTGTC[J/T]TGGTCTGAGATTTGATTATCAGCTGGGTGAAGTTAACCTGTTCTCTGTTTCA

WI-18063	105	G A ---	---	---	AGGCTTTAAACTGATAACAAATTTGCCTTTAATCACATACAAAAAAGCTCTGCACCTTTCATTCCCTTCCTTC CCATGTTTCTGATTTTGATGTAAACTTAAATTTGT[G/A]TCCCTTTAACAATATACGTGAGCTGCA
WI-18078	86	A T ---	---	---	AGTTGAAAGATCAGAGAGGTTATGGTTGGTGGAGTGTAACTGAACTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTCATCCTTTTGTAAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTT[C]GGGCCCTTTTATACCTTCCATATCTCAACTGTTAAGC
WI-18119	38	T C ---	---	---	GCAATCTGTAACAGTTTTGGTAGTGGTATTACAGAGGAT[C]TTGTAAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTGGTCTT
WI-18142	66	T G ---	---	---	TTCAAGATAATTACAAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATAATCTATATACT T/G]CCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68	T C ---	---	---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACAGATTAGTCCATGCCTGGAGGTTAGTCTGGGGG GTT[C]CGCGGGATGGACACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T ---	---	---	TCATCTGAAAACCTTGCTGTAAGCCAGCATGGGT[G/T]GGGAGGTGATTATGGCTGGGGAAGATG GGCACTACCCGACAGCAGCATCTAGCACACAGTGACAGGAGCTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---	---	---	ACAGATGTCAGTTGTTGAATTGGCCCATTAAGATATGGGGCTTTCTTGTAAAAAGTCAATCCAAA AGGCTTGGCAAGAGTTTGCTATACAAACGGAGGACAGAGAAACATGA[G/A]CTGGGAGTAGGCTCT GACAGAAGGTGGGCTGC
WI-18261	26	G A ---	---	---	GATTTGAAGGGATTGCTTTATTTAACTG[A/T]GAAAAAGCGTGATAGAGGAACGTGTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAAGTGAAAGATTG
WI-18268	88	C T ---	---	---	TAGAGGGGAAAGGAGGTGGGTGGCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCTTTACTTCCCCATAGAT[C/T]CCTGACAATGTGCTGCAGAAGCCTCCAACTGGAAC
WI-18299f	107	C A ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTTG[A/G]GAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18299e	101	A G ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTT ATCTATTTG[G/A]GTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18299d	77	G A ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATTGACATATTCTG CAG
WI-18299c	67	T G ---	---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATTGACATATTCTG CAG

WI-18299b	52	GA	---	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTG[G/A]TTGCCAATTTT TTTATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAATATTGACATATTCTG CAG
WI-18299a	48	CT	---	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTG[G/A]TTGCCAATTTT TTTATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAATATTGACATATTCTG CAG
WI-18307	76	GA	---	---	---	TCAACTGTACCAAGTTTAGCAGCAAGAGTACTCTCTTAGAGACTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	CT	---	---	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	TC	---	---	---	ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCATTTAAGAAACACACAAGTCA
WI-18395	77	GC	---	---	---	TCCTGACATGATCTGTGAAATAACGTGATTGGTTGAATTTCCCTGGAAAAATTTGAAGAATAAATTG ATTATTCAG[G/C]TGTGCAATGGTTTATACATATCTCTCTCTTCTTAATGCAAGCTATG
WI-18398	62	GT	---	---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAACAACACTCAAGGGT[G/G/T] GATAACATTGCCAGTATAACCATTAATTCAAACAGCAGCAGAAATTTGGAGGATAATTTGTT
						CTCGTTGGTATCTCTCATCC[C/A]TTCCTTTTCGGCTCTTCTAAATTTAAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAAAAAGAAGTACATATGTAACATTTAACTTATCAACTTGACAAAGTC AATGAAAA
WI-18396	21	CA	---	---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTTCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAGGAGCAGGTGCAGAAAGCTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20	CA	---	---	---	AAAAAGGAAAAAGGATGGAGTAAGAGAGAGAGAGAGAGAGGAAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62	CT	---	---	---	TTGATGTTAATACTGTCTCTGGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATACTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTCCAAACCA
WI-18452	38	GA	---	---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[C/A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	AC	---	---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTATCATACAATGGAAAACTCTTCAGAAATAAGAAGGAA CAAAACCACCTGAATCACACAACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT
EST5b	93	A	---	---	---	

EST5	93 A ---			CTGTGGGAGGAAACAAATTGTGGTATATTCATAATGGAAACTCTTCAGAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGAAAGAAACCAATTCA TAAGAATACACAGTACAT
EST6	48 C ---			TTAGTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTCTTTCCCTTTGCAACAAGACAAAGCCACATTTGCATTAGACAGAT
EST8	158 A ---			GGACAGGACCTCTATCCCGCTGGTCAGCAGCGGCTGATGGACTGAGGCCCGAGGATACTGGGC CTTTCTCAGGGGCTCTCCAGGACCCAGAGCTGTTCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c				TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATC/G/JAGTAGTGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---			TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATC/G/JAGTAGTGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C T ---			CCAAAGTCTCCTGTCCTATAAAGAAGTTTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTGCCCTCATTTTACAGAGGTAGCACAA/C/JTGATTCACAACACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAAAGCCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACTTACTTTACGGGTGTTTTGTTTTCTTAT
WI-18746	114 G A ---			GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAAGAACATACCTTTGCGTGGATCA AGCTGTGTACTTGACCGTTTTTATATTACTTTTGAAATATCTT[G/A]JCCACATTCCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 G A ---			CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCAGGGGAATATGCCAAGG GACCCCTTAATGGAACACACAGATCAGTAGTGCTATCTCATGACAACCAAGAAACCGACGACAAA TCTTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTTAAAGAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]JCTCTTCAACACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C ---			TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCCTCTATAGAAGGCTATCTTAGATCATGT CTCAATGGAACACACTCTCTTCTAGCCCTTACTTGAATCTTGCTATATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTGTAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATATTTT[C/A]JATGATTAGCCGGTAACT
WI-19057i	175 G A ---			CCCATTTATTAGGCCAGTGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTCTGACGGCGGACTTTACCGTGACAGGGAGGTGATTTGTACGTCCAGGCAACCGCAGCCACTG TCTCATGCAGGAACCAACAGTGCCAGATCCCAAGCTC[G/A]JCTCTTCTATCTTGTTTGGCCACA

WI-20103	168 C T ---	---	TGGGACTTCCAACCTAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAAGTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGTCAAAGTCTATATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAGCTGGGTCCTCCCA/C/TTTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---	---	GCCTTACCCATTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAGGACAAGAAATGGA/G/ATTTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTC-TTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---	---	GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGTCCTTAGAAGGCCAATAATAAAGTTGGA/A/GJAAAGGGAGTTTCCACGCAGCAGTGGTGAGC TGC
WI-20613b	156 A C ---	---	GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGTCCTTAGAAGGCCAATAATAA/CJAGTTGGAAAAAAGGGAGTTTCCACGCAGCAGTGGTGAGC TGC
WI-19984	47 A G ---	---	CAGTAAAGAGGTGATTCAAGTTGCAGTAATACACTGACAGGTAATAA/GJTATAACATTAGAAAA GCAAAATTC-TTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---	---	GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCCTTGGAACTGCAACCGACTGCCATGCTGTGGGACTTACACATTCAGTTTGACAGI T/CJTGAANAACCAACTGGAGCTGCTTTTCCAGAATGTTCTGTCTTCAAATAGGAATTCATG TTATTTCTTCTTGGCTTAAGCTCTTATATCTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---	---	GAGTGCCATACCTTCTCCAGGCCTCTGCCCAAGAGCAGGAGTGCCTT/GJAAAGCTGGGAGCGT GGGCTCAGCAGGCGTGGTCACTCCCATCCCGTAAGACCTCCTTCCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---	---	AGCAGTGGCCTTATGTCATGCCAAACCCGCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTGC-TTTTAAAGTAAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGGCGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAATTCCTCAAGGAGCGGAGCAT GTCGTGGACACACAGACTATTTTAGATTTTCTTTGGCTTTTGGCAACC

WI-20146	31	T C ---				TGAGCTCTGTGAATTCATTGAGCAGTTAGCT/C/CATTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAAATCCCATCACTACTGTTAAAGCCCTCATTTGAATGTGTGAATTCATATACAGGC
WI-18922	74	G A ---			---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACATTTTGAAGATGGCATAAACCTGTCTCACCTGGACTTAAGC/GA/TCTGGCTCTAAATTCACAGTGCCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAGGAGCCACACAGTTCTC
WI-18763b	53	A G ---			---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/GA/GTATTTAGAATGTACCATATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38	A G ---			---	TGTTTTTGCCAA
WI-18771b	75	G A ---			---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/GA/GTACGATGATGTGAATTTAGAATGTACCATATTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57	A G ---			---	TGTTTTTGCCAA
WI-18820	70	T C ---			---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAGATGTTGGG AACAGAA/G/A/AAATAAACTGAGTTTAAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18742b	51	C T ---			---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/GA/GATGTTGGGAACAGAGAAATAAACTGAGTTTAAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18882	94	C T ---			---	GGGAAAAATTTGAGACGCAATACCAATACCTTAGGATTTGGCTTTGGTGTGTATGAAATTCGTAGGCC/T/C/JTGATTTAAATCTTTCATTGTGATTGTGATTTCCCTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-19970b	167	G A ---			---	GTCA
WI-19970a	126	T C ---			---	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTGTTTTCACTTTTCGCCAATGTAC/JATCGGGTTTGTTTTCTTGATTATTTAAACGGTTGTGTTTCCCTTTTCCACGGAGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
					---	GTGTGTCAAAAATGGGGTCTGCTCCTGCTAOCCTGACCCCTTCCCTTCTCCTGCTTCTCTCCCTCATCA TCATTTCCCAACAACATCCTCTGCCA/C/TJACACAAACAAACGTAAGTTTCATTTGGGCAAAAAATTGA GC
					---	TATAAGCCCGAGTCACGAGGCGCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCCAACC GGCCCCCGGCAGTCAGTCOCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTGCGGGGACC AGCAAAGGCCCTTCTCACTGGGTTGGTCAAAG/GA/JTAGTCAACCTTGGCCTGGTGCATCCACAGAGGA TGTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA
					---	TATAAGCCCGAGTCACGAGGCGCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCCAACC GGCCCCCGGCAGTCAGTCOCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTGCGGGGG ACCAGCAAAGGCCCTTCTCACTGGGTTGGTCAAAGTAGTCAACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTCAAACCCAGAAATCTTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCCTCCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTAGTCTCGAGAAATGTTGTGAGGGTTATTTTTTAAAGTTCATAAAGAAAT/ GACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCCTCCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTAGTCTCGAGAAATGTTGTGAGGGTTATTTTTTAAAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCCTCCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTAGTCTCGAGAAATGTTGTGAGGGTTATTTTTTAAAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC TGCACATTCCTCCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGT CTCTTGGGCTAGTCTCGAGAAATGTTGTGAGGGTTATTTTTTAAAGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTTAGTATTTTAAAGACAGTCTCAAGCACTAAAGTGGCTAAATTC AATTATGGGTATAGTGGCAATAGCACATCTCCCAAGCTTAAAGACAGTGGATCATGAAAGT GCTGTTTTGCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAGGCTCCTTCATGTGGC GTAATGGGCCATAGCCTATAATGGTTAGAACCTCCTATTTAA/TCTGGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAGTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTAACCTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/A/GTGTAAATTAATTTCAAAATTAAGTCTACAGTTAATTATGTGCATA TAAACCAATGGCCTGGTTCAATTTCTTTCTTCTTAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAATAATATTATGCCCTCTCTCACAGTCAAGGAACTGGGTGGTTGGT TTTTGTGCTTTTTAGATTTATTGCTCCCATGTTGGGATGAGTTTTAAATGCCACAAGACATAATTA AAATAAATAAATTTGGGAAAAGGTAA/GA/JACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAACTGGAATAAGCCTTCGAAAGAAATGTCCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAAGTGTGTTGCTGATTTTGAACCTGTATTCAGTTAACTGTTCCC CTTGGTATTTGTTTAAATACCCCTGTACATATCTTTGAGTTCAA/C/TCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTAGGTGAAGAACGTGCTTGTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---	---	TTTGTGAGTTGCTCTCGCAATGCCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAGGTGAATTTGTCTTCAAGGACATTTGGTGAAGTCCCAACAG ACACAATTTATCTGCGACAGAACTTCAGCATTTGAATTTATGTAATAACTTAACCA/CJGGCTG TGTTAGATTGTTAACTATCTCTTTGGACTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGTCTATTATAAATTCATTAACCACTACAGGTGTTGAATGTTAAAA TGTAAGCCCTCCAGTTTCTTTCAGTTATTTCTGAGTGTGACAGAGCTATTTGGCACTGTATTAAT GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTGTCAATAACAATATTGTGATGCATT TATCTT/CJATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	GCCTCAATTGGCGATTGATTCAGTGGCCACAATGTAAACAGGTTGGTAGTTGTTACTATTGTAAT ATACCTTTTCCCTTATTGTATTCTT/AJGTAAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT/CJGGGGTAGCCATTGTGCAGTATGCCCCGGGGGAACTTGCCAAOCTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A/CJTAGAGGCTGGGGTAGCCATTGTGCAGTATGCCCCGGGGGAACTTGCCAAOCTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTGTGCTGTCCAT/CJGACTGTCTCTTTGAACCAAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCCTGAATCGGGAACAAAGGTTTTATCTAATAAGTGTCTCTCCATCAGTTG CTACCTTACCACACTTCCCTGTGATTTGCGTGAGGAGCTGGCATCTTACTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGTGCGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	TGGAAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAGTA TGG/CJTTAGGGAAACATTCCATCCTTGAGTCAAAAAATCTCAATCTCCCTATCTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	CACGGTCTCTGCATCGTTACCAGAGCGCTTCTGGTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAAGCTTTGGTCTCAAGTCAATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA/CJAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	CACGGTCTCTGCATCGTTACCAGAGCGCTTCTGGTCTAGCCACG/CJCCCTGTATGACCGCGCAA ATATCCCCAAAGCTTTGGTCTCAAGTCAATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCCCTCCCTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	TTGAGGAGGTGGGTGAATGCTCTTGGCAGGGATTTGTGACACTGCAATGCTGGGCTGTGTTCC/T/ CJCGGGCTCTTCTGGACCTTGACCGTGGATACAGGGCATGTGCCATGTTATTTGGGTCTCTGGAGGG TGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCTGTGGCTTATGTACCCCAACAGAGGGGTCTGAGAAAGTCTGGCTGCCTGGGATGCCCTGCCC CCCTCTGGAAGGCTCTGCAGAGATGACTGGCTGGGGAAGCA/GJTGCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTTCTGTGGCCACCAGGCACTAAGGCTTCTCTCTCC AGATGTGCTTTGCCTGAGCAGACAGATCAGCATGGAATGCTCTTTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTGTTTAATATGACATGGTAGAGAAGATAAG GTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCTCAAC/CJCTCAACACTATTGAG TTTTGGGCTGGATAGTTCTCTGTGTGGGGTTTGCTTGTCACCTGTAG
WI-19016a	161 C T ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTGTTTAATATGACATGGTAGAGAAGATAAG GTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCG/CJTTGTATACAGAGGTTCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTGTGGGGTTTGCTTGTCACCTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAGCTTTGGCTAAGGACACCCGGCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACCAACAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTTCCC/CJACTACCACCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACCAACAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTTCCCCTACCACCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCCAGCTCTGTATCCTTGCTTGAGGGTCTGTGTTACGGCCCTCCAGGCAATGGTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCCAAGCTCTAGAGGCTCCA/GJTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTATTTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTTAAGGAGCCTTGGCCTTGCAGCCCAATTCAGCAGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCCTGTCTCTCT CCCCAGTGTCTCACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGAGAAC GGAAGGAAGGGCGGTCATTG/AJGGTATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTAAATGAATAC TTTGTTTGT/CJCATGTTCAAAAAAGAGTATTAAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTGTCCACCCACTCTCGGGCATTTGCTGCAATATTCTGGGCTCAAGTGGGAGGCCACGCTG GGAACAAGGCCTCAGAAACAAGGACATGCAGCTCCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---			TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGATC[A/G]GACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGGTTTCTGACCCCATGAGAGGCCCCCTC ACCCTCTTCAACCTCCTCTACCAACCAAGCTCTCGGCGAGTCATGGACTTAT
WI-19766a	31 G A ---			TGGCCTCAATGACTGGTACATTGGAGAAAGCT[G/A]TGCAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAACAGAAAGGCACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGGTTTCTGACCCCATGAGAGGCCCCCTC ACCTCCTTCAACCTCCTCTACCAACCAAGCTCTCGGCGAGTCATGGACTTAT
WI-20512d	126 C G ---			CTTCCTCTGTTGGCTTTGCATTTGTGCGATTGGAAAAACCACTTGGAAAGGGGACTTTCTCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA[C/G]AAAGC TTAGAAAGGAAGTAAATTGCTTCTTTGAATATGATTTAGGGCGGGGCGTGGGTGGGCTCAGCCT TATTAATCCCAGGCACGTGGGAGGGGCAACGCGGGTGGGATCACTGA
WI-20512c	59 T G ---			CTTCCTGTTGGCTTTGCATTTGTGCGATTGGAAAAACCACTTGGAAAGGGGACTTT/GTCTCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAAGTAAATTGCTTCTTTGAATATGATTTAGGGCGGGGCGTGGGTGGGCTCAGCCT TATTAATCCCAGGCACGTGGGAGGGGCAACGCGGGTGGGATCACTGA
WI-19599	230 C G ---			GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTACAGAAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGATGGCTCGGTGAAGTCTTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACAGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGCA[C/G]TTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---			TGTTTGAATAAAAATTTCCATGGTCTTAATTGAACCTGTATGTTACTTTCTTTTAGAATATCCTTTT TTCATTAAAAATAT[C/G]CTAAACCACTCTATGTTTCAACCTTCTGTTTAAACACTAAGATATGGT TTTTGAAAGGCCACAAAGTCACCACTCCATGAAGTGGGCGAATGGTCTTTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---			CCAGAAATAAGCCTGAATATCTCTTTCT[C/G]TAAAAATATAATTTTCTCTTTGCTCTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTTATACCTTGTCTGTACTGTGGAAATCAACTAA
WI-20341	221 G C ---			TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTCTTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAGCTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTGGGTGACGTATGC ATCCCCCATGCAATTGGTTT[G/C]AIGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60 T C ---	---	---	TTCTGGTACATGGTAACTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGTCGGA AACAGTAAAGCAAATTACCAACAATTAGGAGGAATTTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTAGCAATAAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---	---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTCCACCCAGGAGAACACTTGACTTCATTAAGGCAAAGCCTTTACTCTGTACTCTTTTCCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	---	CCTGCAATCACAAGAGTGAAGTGTGATATTTTGAAATCATACTTGATTTAACCCACTTCAGAAA TTCTATT/CJAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161 A G ---	---	---	CTGGATTTAATATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATCCCTAAGTAAGTATTGACGACTGAGACTAGTCCGGCAA GTCATGAGACCCCTTAGCTGATCTCATJA/GJAGTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGCGATGAAGAGACTGTTGGTCATGGCGGTGA/CJGTCTCTTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTGTAGAGCTCTCTC
WI-19348b	98 G A ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGCGATGAAGAGACTGTTGGTCATGGC/GJAGTGACGTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTGTAGAGCTCTCTC
WI-19635	98 A T ---	---	---	ATTAGTTCGTGTGGGCCACATTCAAAGCCATCCACACAAGCTCTTGTAAGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTATATATCTTATGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCCTT T
WI-19641a	46 A G ---	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATGTGATAAGCACTAG/JGTATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATGAATGGATCAGAGTAGTAAGTCAAGATAAGTGCATAATGTTGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTAATTTTAAATTCACCCACCTTG
WI-19642b	52 C A ---	---	---	ATATAGAGTACCATCCATGGTTCAAGCATGGCTGGACACATTTATCCCCCT/CJAGGGTAAACCCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGATGGACACAAAGTTTTCATGTCATTA
WI-19673b	180 C T ---	---	---	TCGCGCATGATCACAATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCAATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAAATCTAATAGT GAAAGGGCAAATGATGCTCAGTATCACTGTGAAACATTTTTC/CJCTTGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACAGCTCAAAAAAACACAGCCC

WI-19673a	35	G A ---	---		TCTGCCATGATCACATTGTGATGAAGAACAATGATG[G/A]TCACATAGTAGGTAACTTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGTCATCACCACTGTAAATCTAAT AGTGAAGGCAATGATGCTCAGTATCACTGTGAAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCTGAAGGCTTCAAGGTCCACACGTCACAAAAACACAGGCC
WI-19724	35	A G ---	---		TTTATTTGGGAACAAAGGATTGTAATTTGGTAA[G/A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196	T C ---	---		TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCACAAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTTCTGGATTGGCTTCATGAGAAATGGTGGCTTGGATGGAGGTGACATTCCTTGCTGT GGTGAAGTGAAGAAAGGAAACACAGCAATGATTCCATAGAGGCCCTTTAAAGAGACCCG[G/C]TGG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAACAACCTCTTTGGCTG
WI-19269	85	A T ---	---		CTTCCCTCATCCCTCTCCACCACACATCCCGGAACAAGTGTCCAGGATCCCTGCCCACTGGC CATTTTGGAGTGTCC[A/T]TTGGGTAGCAATGTGGAACCAACCCAGGCCCTTTGTGGAGAAAAATGG AGGGGTTGAGGAGTCCAGAGGGGCTTATTGAGGCCCTTTGCCACTTGCTCATAGCGGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGGTAGGCA
WI-19946	122	C T ---	---		CAATGGACTGAATGAGTGCCTGGTGGGTGGGGACACACACACTTCAATACACGTCAAGGTGCG CTTCCAGTTTTAGAAACAGAAATCTGCATCTCAGCTGAGCGCAGAGAGGT[C/T]TCTTCTCTG ACCCAGACGCACTCACGAGCGAGTCTGGTTTCAAAACTGCATTTAACCTGGCCAGAGAGTTCAAC CGTAGGCATCTTTAATAAATACTAACCTCCAGCAAAATGTGGTACGGTTACTAA
WI-19956	141	G A ---	---		CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACTTTACAGCACACATTTTAGGCCAAGTTTGGATCTGTCTGGACCT CAATG[G/A]CTCTCGGAGAACGACCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCTCAA GTGATGGCCAAACAGAGCTTCTGAACCTCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---		TTGGTTGGATCTTGTCTGAAAAAAGCAGTTTTAA[G/A]GTATTCAAAATACCTTTTAAAAA GTATCTAGCACAAAGATTTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTGCGCTCCTGAAAAACTGCAGA AAGGCACCTTGAAGCTGTTTCTTTAAGATATGGGATTTCTTTTATTCTT
WI-20218	26	T C ---	---		CCACACACTCTGTTTTATAAGCTA[T/C]JAGGACAGAGCAGAGATGGAAGTGAACCAAGGAGTAG AAATTAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGATGACAAAGCCACATGTGCCCA GTCAAATACITTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATCTACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---	---		CAACCTTTTGAACAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGATTGGGAGGGCTGGGCTCTACCCCTTTCTTTTCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGCGGGAAGCCAGCTCTCCAGATAGCCACTGTGG GTCCGCTTCACCTTCTGTCGACTCTCATGCTGGGACTTGTCTTTCCGGG

WI-20361a	192 G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAAATATGTGAAATCTGATGTGCCAGAGTTACACTCTGCACCTCCAAAGCTA CAACAGTCCACAGCTGAGAGGTTCCCTATCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACAGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75 A G ---	---	GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTCTTCTTCT TCAGAAAT[G/G]TCATAAAACATCATCTTTTACAACATGGAGAGCGAGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAAATTTTAAATTTGTTTAAATCCCAAGGTGCCTATTGAATCTTCCAAAATA AACTGCCATATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 G A ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACITTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTTCCCTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCAATCAGG
WI-20593	79 A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTG CTGTACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAAGAAA AGCTGTAAAGGAACCTCAGGATGTTGTAGGAAGGGGAGTGGATGCCAGGCTTCACCAGACTAT CCAGAAAGCCATTCATGGGTAATTTGGTCTGCACTACTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTTGTCTCAT/C]ATGTATCT TGTCCCTGCTGCTTTTAGGTAGCAAGGTGTATGAATCTTTAAGTTTGTGTTCTTTTCTCCTCGT GGTATCAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAAATGGCCATGGAAGTGAAGC AAAAGGCCACGTTGGGATAAAATCACTCACCATCGACGCCACCAAGTAT
WI-19066i	239 A G ---	---	TGACAAAGGAGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGGTTGGTCAACCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTA
WI-19066g	184 C T ---	---	TGACAAAGGAGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGGTTGGTCAACCCTGTAGCTGAATTAATCTTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTA
WI-19066f	148 T C ---	---	TGACAAAGGAGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGGTTGGTCAACCCTGTAGCTGAATTAATCTTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTA

WI-19066e	147	GC	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCG/GCTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066c	100	GA	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066b	87	CT	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/GCTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066a	72	CT	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/GCTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-20660	105	GC	---			TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTG/GCTTAAAGGGAAGCATTAAATATTA CAGACATAATTTACAAGGTTCTGAACATGAGTGATTCCATGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCCGCCCCCAAAAAATACTGTTTAAACAACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCCTGCTGCATGCATGTGCACCCCTGGTTC/TCTTGGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	CT	---			TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAAATGT/GTATTAACTTCTAGTTGCTCTTGTCTTG GTCTTCTTCCAAATGATGCTTACTACAGAAAGCAAAATCAGACACAAATTAGAGAGCCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAAGGTGTC AGTGCCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37	AG	---			GAAAGCCAGAGATTAGCCCGCATTCGGCATCTGTCAACCAGGACAGAA/GT/GCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTTGGAGATCAGAAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTTGGGAATGCTT
WI-18790	49	AT	---			AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCCTC/G/GTGGCCAAAGCCAGACACTCAACCCACCTT CCCCAGTGGCCCCGTGGATCTGCTGCTAGGCTGGACAGGATTTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTTCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA
WI-18987	35	GA	---			

WI-18919	26	C	---				TGGATGAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCAATTTTATAGTTCACTTTCTCTACAGTG TTGTTTTGTGTGGTTTTATTTTATATACTTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64	G	---				CTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G	---				CTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCA[G/C]JACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T	G	---			CTTCTGGTCAAGGCTTTGGACAT/GJCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G	A	---			TCAGAAAGCAGACATGGCATCTGTTCCCTTGGCTTGTGTTGTTGTGTACCTTTACGAGACCTGAATT TTAGAAATTGCCCAGTGTGCCAGAGTGAGTGAGTGAATTTCTCCTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAAACATATCAACCA[G/A]TAGCATTAAACCCATTTATTTCTGTCTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T	A	---			CCAAATTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT/AJGTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCTATGGAATGCAAGCTGC ATAATTACACATTATCAAAGTCCCTTTACAAATTTATTTCCGCAGCATGTCAAGTAAGTAGACCCA ATGGGGAGAGAAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210	G	C	---			CTGTTGAAGGCTTCTCAGGCAACTCCAGCTTAAAGCCCTAGACAGGTAAGAGCACACATTGGATG GCAGCATGGGTTCTTCCCATTTTATGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATATT CCTTTGCCAACAGCCTCACTAAGAGGCTTTTGTCTGAGTCAAGCAACACACTTGCTGCTCTGCC CTTGGAG[G/C]TGCAATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T	C	---			TTGAAATCCAGTCTCCTGGCCCCCAGGCAGGCTGTCAACCATAGATGTCTTCTCTACTGGGGTC GTTCTGGCTTTTGTTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTTCTGTTATCTGAAACTGGAACCTGAACCAAGTTTGCCTTCTCTAGTCACC AAGCATACTT[C/T]CTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T	C	---			GTCTCCCAGAGTCTTCTGCACCCCAGCCCCCTGTCTGCTGTAAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGGCTTAGTTTGGACATGCTGGTAGGACTCCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCATCCTTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAAAATAAAATTAGTGTGCTCTTGCCTGTCTGT
WI-19135	20	G	A	---			CAGTTACCCCTGCTTGGCTC[G/A]AAAGTGTATCAATTTGTAAATTTAGTATTAACTCTGTAAAAGT GTCTGAGGTACGTTTTATATATAGGACAGACCAAAAATCAACCTATCAAGCTTCAAAAAC TTGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTTGGCCATATAAATGCTGATATTTACTGGAAACCTAGCCAGCTTAC

WI-19236	54	G A ---	---	TACACAGAGGTCGCACCTGGACTCTGAGGTTGGGTGTGGAAGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCAGCTCTCTGTAGCCGGTTACATGGGAACAGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACTCTCGGTATCTCAGGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTATACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTAGCCCTTGTGACCTCCAGCCCTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTTCTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGGCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAGACTGAACAACGTTATTTACAGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAGACTGAACAACGTTATTTACAGAGGGTAGA C/TGGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCCCTTGTGGGTGATGATCAGTGTGCTGTG[C/G]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTGTCGTAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCGAGTATGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[G/G]GCTTCATGTAAATATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTACAGTGTCCAGCCGGTTCTGCAGCCTA
WI-19222	179	C T ---	---	CGTTTTCCTAACTCACCCAGTTTAGTTGGGATGATTTGATTTCTGTGTTGATCCCATTTCTAA CTTGGAAATTGTAGCCTCTATGTTTCTGTTAGGTGAGTGTGTGGTTTTTCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCTTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAAGCAGCATT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCCTAAGACAAGAACATTTCTCATAGAACAATTG ATCTGTTTACAGGAACAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A/GGTAGCTATTTTTTCCCTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTTTCATACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	C T ---	---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTTACACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGCAGCCCGAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAGCAC TTCATCCACTTGTCTCTCCCTACCCCTCGGCACCCCTGGGTGGGAAGGG
WI-19134a	162	T C ---	---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTTACACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGCAGCCCGAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAG CACTTCATCCACTTGTCTCTCCCTACCCCTCGGCACCCCTGGGTGGGA
WI-19224	112	C T ---	---	---	GGTTTACCAGTCTTCCAGGGAACTCCGATGAAGTGTCCACAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAAGTTGTTCAATATCCAGCAGGCCAGAAAGACTTCC AGGGAACCTCATTCAAGGAGGTGAATAATGATGGATGACTCTCCAAAGATGA
WI-19201	179	T C ---	---	---	GCAGCTCTAAGGACCCTGGCCATTAGCTCTGCTTTGATGGCATTCCTTTCCACCTTGTCTCTC CTTTGCTCTCTGTGTAGTGGCAGGTATGACAACTATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCACTTTGCCCTGCAGGTGCACCGAAAGGAC/TCTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAGGTGACAGCTCCATGCTGCTTGGCCTCAA
WI-19034	45	T C ---	---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGTGATGAGGATAGGGAA/TCTACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAAAGGTTTTACAGTGTCTGTCTGTTGAAAGTGAATATAAATTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTCAGCATTTAAGTTCTGTCGAATTGAC ATTTGCTACTATATAAATAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25	C G ---	---	---	TGTTCTGAGTCAGCTGAGGAGAG/C/GTCTCACTCAGGAGTTGATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTGAAAAGTCTAGAACTCCTGTAAAGTTTTGAACCTCAAGGGGAGAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---	---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGATCATCTCCAGTCCCTCACTGGGGAA/W GJAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G A ---	---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGATCATCTCCAGTCCCTCACTGGGG[G/A]A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T C ---	---	---	GGCAGCAGCTTTTTTAATTGAACACTTCTCTCTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCCTCACA
WI-18501	121	C T ---	---	---	CAGAGGAAAAGTTTATTGATCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGGCAGGACAGAGGGGGC[G/T]GGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87	C A	---				ACAAAGAAATGGAATAGGTTGCGAAACCTTATCTGCATGTACAAAGTAATCCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATTATATCTCTTTGCAT CAGAGCTGGTGGAATAATCAT
WI-18148b	101	A G	---			---	TTATTGCGTTCTTCGATAAACCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTTCAGAAACNTCGATTCTGAATATCC[C/A/G]TGGCGGCGATATGCAAAGGAATGA
WI-18254	64	T C	---			---	TATACGGATCATGTATTTGTGTGACCACCACCTACACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]GCCAAATCCCTCTTCTTCTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117	C A	---			---	CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGCGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGTG[C/A/G]TTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40	C T	---			---	ACCACACATTTGTTGAGAGCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T C	---			---	GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTACACGGGTGGGAGACACAAAT/ C]GAGTAAATAACAACATAATATTTANATGACAGTGCAATTAATAACGTCCTGGGTAAAGCCAGAG GGGAGGAGGGGCTCTTCA
WI-22585	56	A G	---			---	TTTATTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCGAGGTATCCTTCAATTTGGCACAGCTGTATAGATTGA
WI-21155	36	A G	---			---	GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC[A/G]TCTGTAGAAATGATCTAAAGCTTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			---	GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGCAGCACTTCTCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAGA[G/A]GGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTTCACACAGACAG GGAAACAGGC
WI-19888a	98	C T	---			---	GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTATTTTGATATGATG AAATATTTTGGAACTAGAAAGTAGCAGTG[A/C/T]TGGACAACGTTGTAAGATATTAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTGTATTTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---			---	TGAGACCATCCTCTCAACAAGAATCAGTCAGTTCAGCACTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C/T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			---	TCAGAAATGCTTTCCACTGCCCCCAACCAAAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTGGAGGTTCATGACAGGATTAGTCTCTCTGT[T/C]CTTGGT GCAAGTTTGAACCAAGTATATGTAACATTGCATCAGAGCATCTGTTTCCCTGTGAGATCCCCACTAG

WI-20561b	94 T C ---			CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACCTCAGATGAAAAATCCTTACATGTCGCGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---			CGTTGCTATTAAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATT TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---			GCTTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/AJATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAAITTTCAACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116c	59 T A ---			GCTTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGA CATATATAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAAITTTCAACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116a	22 C G ---			GCTTTCATTTCTGTCAACCCACCGCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAAITTTCAACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20466b	133 G A ---			AAAGATTTGCAGTCCTGGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAAACAG NTCCCAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAAAGTGAACATAATGAAGTGAATAAACGC G/ATGTGAACATAATGTTTAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTTATTCTTTGCTCTTTATCCCTTTGAGGTTGATT
WI-21444	39 A G ---			CTGGGACGCAAGTAACCATTTTAAAGAACTACTCTCAACG/AGAGTTCTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACCTTATTGGAACATACTCTTTGTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGAGAAAGTGGTATTAGAGGATACAG CATAAATTTAAATGTAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAAATTACTGGTCATGG GAGATTGGATAGATTCG/CCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---			GGCGTATTGTGCAATGTCCACACAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGACTCATAATTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAAAATGTAGCATTAAGTGGTATTACTTGAGGGCA ACA/G/AJAATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45	A T	---	---	CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTAT/TAJAAAAAAAACTATAGTCTG CAGTCTTTGACATACCTCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCTTTTGAGCTTAAGTCTGTTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTGTGTAATTGCTG
WI-21778b	155	T C	---	---	AAAAATCCATAATTATTGAACCCAAAGTTACAGAGAAAGTTCGTAACCTTTTATTGAATTAATTGAC TCTGCCGGCTGCTGCTGCTTTCAACTCCAGTCTGTCAATGCCCTGTGAGTGGGTCCTCCAG GTCTGGGCTTCTGAGGTCTTCGCTAGAGGGGAGGGCAGGTGGT
WI-20907	241	A C	---	---	TGAGTCAGTGTGAGATGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAACACTGTGCCTCT CAATGATCTAGAGCTCATCTTTGGCGTACATGAGGGGAGTTGTTGTTCTAGTACCCATTTAGCCOC ATGGCTCTTCAAGCCAAATTCACACTGGGAAAAACACACCTCACAAGATGCCTATCCCATTTGAGTTC ATACAGGTTTATAGTAGCTAGAACTAAAAAACATTTTAA/CJAATTATCTA
WI-21449b	222	C T	---	---	AACAGCAGCAGTCACTTCCAAAATGCAAAAAAATTACAATTTTGAATAAAAAATTATAATGTTTA TAATGCGGGTCAGAAAGANTTGAAGGTACAACAGAAATCAAAATCACGCAGCACTGGAGGCGGTGGAG AAGCCAAAGCCCACTGGTCAGGGTCCAAAGCTGACAAGAGTCCAACTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTJGACAGAGCCAGTGCTCTGGGTTAG
WI-21558a	157	G A	---	---	GCTTACAAGAACCTGTGACAGCGAGNTGGGTGGAACCGACTCCAGCTCGAAACCTGCCCCTG CCATCCCTTTAGCGCTCTTGGCTTCCGGCTGATTTCTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCTAGGGCTGCAA AAGGGCCCCGTGAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178	G A	---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCTTGGGCTGACCAATGGGTGATTACATTTAAAAACCAACCAAAACAAACAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/GAJAAATTCATGAAAAATTCOC CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110	C A	---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCTTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAATTTTATGAAAAATTCOC CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146	G A	---	---	TCATGAATATGAGCTCCATAATCTTCTCCCTTGTAAACAACTGCAGTCCGTTCAACAGCTGTAAA AACAAAGCCCAACCAAGACATCAAGAGGAGCAAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/GAJAGGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGCCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTGTAAACAAAC/C/TJTGAGAGTCCGTTTCAACAGCTGT AAAAACAAGCCCAACCCAAAGACATCACAAGAGGAGGAGAGAGTGGCAGTGAGAGGAGGAGCCTGTGTA AAGGATGTTTCAAAGGAGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---			ACATTCCGAGCCAGTCTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAAGGGTCGTGATTGATTGAGCAATCTAGGGG/A/CJTATGTGACAG TTTC/GJTGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAAGGGTCGTGATTGATTGAGCAATCTAGGGG/A/CJTATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGACTTCTTG/A/GJTTC TCATACAAGACAAGCACAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI- 18829b	35 T A ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG/AJAATAACTTATGTGACTTCTTGATTCA TCATACAAGACAAGCACAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-20964	87 G A ---			AGCCAACCTAAGGCCCAAAAAATTTCTTAATATAGTTATTATCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/GA/GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGGAAGAAC AGATGTTAAACAAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---			CTCTGAACCTAAGGGCCGTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAAT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTAACAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---			TGTTTTGAGGGCTGTAGCAGACTACATAATAGCGGTGAAAGCGGCTGCCCTTCCCTCTCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGATGCAATGATTACTAGCACTAGGAA GCCAACGGGAANAGACCCCGCGCTTGTCTC/TJGTGTTTAAATCCAGGTTAAGCTATACACGTTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCACTCCCTGCTGATGGGAATGAC

WI-21661	117 GC ---				GCTTAGTCTCCACCCCTTTAAATGTAAGTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTCCAACTTTAGAAATGTAATAAAGAAATGACATTTTAAATAAAATA[G/C]TTAGTCACAGTCACACAAACTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTTCAGCTATGAAGGA
WI-21980a	25 TC ---				TCAGTTTAAACACATTTCATCAAGGA[G/C]AGATTAAATTAATGTCAGGTGAGCATAAAGGGAGATTATAAACAGAAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTATTTTCATGGGTGAAGCCCTCGGATAAAG
WI-21636	71 AG ---				TGCTTGATTAATGTGGTGTACATTATCCTATTTTCACAGATGGAACAGAAAATACCAGCTTTTAAAG/GTTAGCAATATCTATTATAATAATTTGAAATAACACCATAATAATATCACTAAGGAAGTAATCTAATGTGTTGATTTTGCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112 GA ---				TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGACAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACAG[A/C]CAGTTAATTAACATAAGGAACAGAGTCCTGCATTCTGAAGCATAGGATGGGGAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCCACTGAACCTCACCCAGCTGAAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97 CT ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATCTTAAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGAGTTGCGGTGTCCTGTCAGAAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGAIG
WI-21524a	35 AC ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATCTTATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGAGTTTGGAGTTGCGGTGTCCTGTCAGAAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---				TTACCTTCCAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTAAATCAATAAGCCAAAGACAATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCTGCCACAGAACCCTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTTCTTAGGG
WI-21703d	197 AG ---				CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGAGGGCTCTGCATCCCTTTCTCAGCACAGCACCATCTTCACCCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGGAAAGAGCCTAGGGATCAGAGGATAGAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCAGCACAGCACCATTTCACCTCCTGGGAAGCAGCATGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI- 22663c	139 G A ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGCGAGGTGAGCCGGCGCTCGCTAATCTTATTC CCAGTCTCGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTACAG GC[G/A]GAAGAGCTTCTCATTTGCTGAGGGCTTTTCCTGAATCCGTTGTAATGTGGGT
WI- 22663b	55 C T ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGCGAGGTGAGCCGGCGCTC/TGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCTGAATCCGTTGTAATGTGGGT
WI- 22663a	38 C T ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCAGTGGC/TGAGGTGAGCGGCGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCTGAATCCGTTGTAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCTGCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACTAACAATAATAGTTTCTGTAATATT[A/G]TTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI- 22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTTCGAT/CJAGCACCATTT CAAGTTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157 G T ---	---	AATCCACACTTTCACGGAGGGGAACAGCTGCCATGTCTCCAGGCTCACAGCAGCGGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCAAG/GTCCGCTTGAOCAGGTGATGGCTGCAGGGGCGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTTACATTTGTAGAGAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCCTCTCCTGCTAACTCTGACAGGAGTGTGGGAAACGAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]TGTAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGGCCT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCGCAGTCGTCGAAGCCATAGTTGGATGGCAGACTTTTCCGGCAGAGGAAT AGCAAGTGCAAGGGGCTGAGGGAGAAATGAACTTGGGCTTGTCTACAGGGTGAAGGCGGCCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGAGTGTAGAGATATAGGA CAAAATCAAGATTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATAIGTTGGGAAT
WI-22750	48 G A ---				TGTAACCTGTGTTTCTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[A/G]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTACGATTCTGACCATTTCTGACTGIGCT
WI-22775a	60 A G ---				TGCTGTTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTCAATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---				CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[A/C]TAGCAAACTGATTAAAGAGAGTAGGTATAAGAAACCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---				TCTCTGTGCTTGAGCCCTCATCCCACCCCTCCAAAGCCCTCATGCCACACACCGTGTCCCACATT CCCCATCCTCCCTGCTGCTCCCATCTCAAGTCCAAATCCAAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAAGGAGGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCGCTGTGGGTC CTG[A/T]TGGCGTGGTGATGTGGGGGCCAATCCTTGAGGCCAGAGGTTCA
WI-21031	31 C T ---				TGAAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCCATTGTTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---				CCATATCCAGTCTCTTTGAAGCTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTTTATTGTTTCTCCATTTCTGTCAAACTTTT[C/A]JTTTTGTTTATAA ACTGTTTCTAAACTCACCTTAATCTCTAICTGTATTNCTGTAGTTCCTGAACTTCTTTAGAGG
WI-21186	95 G A ---				AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCCAAGAGCTTCT GATTGAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTCCTAAGTGTGCAG ATGCTGCTTGTCCTGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTCTTTAAA GGAGAGACAGGAATTCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94 A G ---				CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	---	TTTTCCCCACATACCAATGCACCTGTTTGTATAAACTATT/CJGTGGGGTAAGCCCTTCITTTGGAGAC CAGTGACATAGACATGATCCCATTTATTAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	---	ACCATGTGCATTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAACGAGTCATTGAAAATGCTGACITATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	---	ACCATGTGCATTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTCTCCTCAGCAAGTC[G/T]GTCCAAACCTTC CAAAAGAACGAGTCATTGAAAATGCTGACITATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACCTGAAATCTGTTCAAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTTCTGGG TCCAATCACATACTTCAGGTCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTTC/TCTACTGAATCTTGGTGGGAG
WI-21122a	42 C T ---	---	---	TCAGTTTGTATCATAAATCCCCTGTAAAAGCTAAAGTTATTCA/C/TJTTAACAGGAACTCTGTTTTCC TTATTCAAATGTCACAAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACTGGAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---	---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGCGGGAACCTATTCACAGGAG[G/G]CAAGGAGAAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	---	AAGGAACTGCATGGGTACAAAT[G/T]TCCAAATTCATACCTTAACAAGGTGGGAAACGGGTCAATTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	---	GGACACAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTGCATTTCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTCACTGAAGTCAATTCCTATTCT/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTGCATTTCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACCTGAAGTCAATTCCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442	37 T C ---				TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAGGTGGCACAATTTAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43 T C ---				GTGACAAGAGGTGAAGCAAGGGACAAAGGGGACAGGGCGAGTC/TCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---				ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTA ATCAACGTTAAATTTTGTCGACCAAGTTCTTCTGCTGATCATTGATAATGACAGATCCAAACAT GAAACTCCTGAAGCAAAATGAATATTTACCTTGCTTTCATGCAAAATTTAGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACACAGATCTAAGGAATTTGTACAGGGATCTCT
WI-21149a	167 G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTAAATTTTAAACAATGACCTTATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACACG/AJTGCTTCAGAAATGCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---				GGTGTCAACTTGAAATATGGTTTAAACAGGATAAGCATTAAAGGAAAAACACTTTCATATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCCGCAAGTGGAGTTTCATGCTCGGTGAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJGAAAGTATTCT GAACTGAGCACGCACTCATGTCTGCATGGGGAACCTCTGGGGAAGAGCCT
WI-21382d	125 C G ---				CCATTGCAGTCCAGAGATGAGAAACTGGACAGAGGCAATCATGAACAGACGGAGTCAAGAGA AGGGGTTCTAAGATGGAGAAAGTGGGGGGGTTTGATCCAGTGGGATNTGGTCCQ/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCATAGTCTCGCAC
WI-21437a	201 G A ---				TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAAGAGGGCAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATCTGTGGGGCAGGAACATGCCAGGGTCTGTGTAATGGCAGGGTCACTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCCCTGGGGAACAGT
WI-21202b	156 A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCA/A/CJGTCTACATGATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGTA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGATTGACCAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTAGTCCCAACTTGATCTCAAAATTCACCTCTTGTCATGTAAACAAGCTCAITCCCTCTAAAGTT TCAGTTT[C/J]TCCACAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTCCTTGGTAA CTGCCTTCTGCATTTGTCTCTGAGGTTGTGTCTCTAGGACTAGGACTAGGATCTCTCTTCTTCTGCT TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---	---	---	CGATGCTGCTAAGATAGGAGTTAATCTTTACATGGTGAGTGGTTCACAGACAGACATCAAT C[G/A]TCTGTTAGCGAGAGAGACACTTTAAGTGGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGCTGGCTTCTTAAAAACAGTAACCAATCAAAAAGAAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAAATGTACATGTAAATCCAATTTAACAGATCAAAATTTGTACACTAAGTTTCAC TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACTTTAAAGAACATTATAAAGGTAATT AAAACTCTAGGTGTACTTAT[C/J]ATGGAAGTGTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAAACATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGCAAAATTACAGTGGGGCAGCGCGTTCGGCTCCAGCTGGGTTTTCOC AGATGCAACAAT[C/J]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	---	CTGCACCGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGACCGAGGCCCTGAACCGGGCAGGGAGGGGAGAGAA[C/G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGSCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGOCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGGCTCTTTGGAGAAGGCA[A/G]AAAGGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTAATTCCTCCCTGAAG

WI-21475b	117 A T ---	---		TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTCTC/TCTTCTGCTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGCACTGGCTCTTGGAGAGGCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCGTTCTCCACCCTATTTCTCCCTGAAG
WI-20893d	207 A G ---	---		TGTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCCAAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTTCATCACCCTCC AGGTGAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/A/GJACATAACATTTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI-20893c	179 T C ---	---		TGTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCCAAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTTCATCACCCTCC AGGTGAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTCAACATAACATTTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI-19941c	71 C G ---	---		GAGCTAAGGGAAGACCCCTACCCAGATAGGGACTAATCGAGGGTGGAGGAAACAAGTGAAA GGTATC/GJGGTCTGGTGAGACAAAGCAGGGGGCCCTGAGAACACAGAGCAAGGTGGTTGGAG GGACACAGCAGGGTGACGAAAGGAGATGGGGACATTTCTTATCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAGCAAAAGCG
WI-21552b	166 C A ---	---		TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACCTCTTGATTATTTAAAAATGT/C/AJAATTAATTTATTTGAATTTAGTTACCCC ATTGTGCTATCAATAATTCATCTTATTCATCTTTGTAACTATTTATTTGTA
WI-21552a	66 G A ---	---		TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCCTTCACTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACCTCTTGATTATTTAAAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACTATTTATTTGTA
WI-21512	54 C G ---	---		TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGT/C/GJTAGAGAGGA AAGAGCTGGTCCCTGCTCTGGAGGCAACGTCAGTCCGGGGAAGGCACCTCGTGTCTGTGATCTGT TCAGTATGGGAGGTCTCCACTCGCCCAAGGAGCCTCGGGCCAGAGATGAGAAATATGCTGTAA TCAGTACAGGGGCTGCTGCTGGGGTCCCAAGAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---		CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCCTAAGCGAGGACAAAGCAACTTCCATT ATTCTAGTTTAGACCAGAACTCTTTAATTTTATTTCTCTTTAATAACTGTCAAAATACACCAAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCGAGTGTAA[G/AJAGTAG TATTCTCTACATACCACAGTATACAATGATGCCTTCTCGAGGTTTAGGAAC

WI- 21514b	133	C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTCTAGGAGCTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGCJC /TACAGGACTCCAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGACGAGAAATAAATGAGG ANTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100	A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTCTAGGAGCTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGACGAGAAATAAATGAGG ANTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	C G ---	---	ATGAAACATGTTGCAGTGGGATGAATTC/GJTTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113	A G ---	---	TTATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTACAGACATAAAAATTTAACATTCT/GJTTCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCCAGATGTACACAAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141	A C ---	---	ATACACAGGCCACAAATTCAGGATGGAAGGAGTGGGCACTTGGAAAGTGAATGACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACCAGAAAGTTTCTGGGGCATGTGATGGCCAGACCCCTTTCCAA GGGAATA/CJTTACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTTCAAGNTTCAAGGCCACAGCAT
WI- 21574a	235	C T ---	---	AAOCCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTCCACTGATCTGGCAGGTGACAGCTCAAGTGAACAGCGC TCATCACTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCCJTCJTGCTGTCAGGTGGGA
WI- 21644c	151	T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACTCACTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCAACCATANTATTTAACAGACTCAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA/TJTTCAATCAAGATCCATGGAATGATGCAGTTTAAATGTGTTCTCAGC TTGCCTACTGACCACCTTTCTCTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55	G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATC/GJTTTAAACA AACCTCATTATGATCACTGTGCAATTTCACTCACCTAAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTCTTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151	C T ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATATTAAGATAAGGATGGACT CTTTCAGTGAATTTATC/TIAGGACACAAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATATTGGCCAAAGGGGAAAGGTAGGTGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATCTTTGAAGAAAAAAATTAJGT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCT TACTGTGTACCAAGAAAGGAGGAGGAGGAGCTACCCAAAGCCTAACCTGGCC[C/T]TGTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATCTGCGGAACTGGGATGCAGGGAGAACCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAAATATTTGTGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTT GTCTGTAGGTTCCAGGGCTGGGCACAGAGGTGAGGGAGAAATNTGGGGTCCAGTGGATCTCCCC ACAACTTC[C/T]TCCAGGGGCAGGATTTCCACCCAGGCCCCAGGGTGCCCCG
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAAATATTT[C/G]GTGGTCCATGTGGTTTGAAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTC CTTGTCTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGAGGAGAAATNTGGGGTCCAGTGGATCTC CCACAACCTTCTCCAGGGGCAGGATTTCCACCCAGGCCCCAGGGTGCCCCG
WI-21760c	81 C A ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTCTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGI/GJGGTGTCTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTATTATTTCTCTTTGAGGAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAATCCTTTTCTTACCAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTACT[C/G] AGAGACAATTCATAGTTCATAATCTTTACGGGTTGTCTTACTTGGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCAATCTTAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGTCAAAATATTCAAATGGCCTGGCAGTGTGGTAATTCAGCAGAG AAACAGCATGAGAAAGGCCGGGAGACAGTAAATAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGCCCATCAGAACATAGCATCTATACCTTCGAAACCT[G/C]CCTCTTAAC CTCTCCAGGCAAGAAAGGAAAAAGTATGATCATATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGTCTTATAGTATAAGAGGGCTTGAATATAATGATGATAAATGGTAGCCCTTCTGGA AATAATTTTGTAACTCIGTTTAAAAAGATTTTGGATGCATTGTCCCCA

WI-21961c	200 T G ---				AGCTTTGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTATTACTTTTATTTTCCGTAAGTTATTGGGTACAGGAGGTATTGGTTATATAAGTTCTTTAGTGGCGATTGTGTGATTGGTGACCCATTACCAAGGAGTACACTGCACCATCTGGTCTTTTATCCCTCGCCCCIT/GJC
WI-21961b	73 G A ---				TCCCACTTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCG AGCTTTGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTACTTTTATTTTCCJG/AJTAAGTTATTGGGTACAGGAGGTATTGGTTATATAAGTTCTTTAGTGGCGATTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATCTGGTCTTTTATCCCTCGCCCCCTCTCCCACTTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCG CCCACCTTGGGTCTCTTTCAAGTGAATJ/GJTTCCCTTTCGTTCTCTTAAAGCCCTTTTAAATGAACCTCCATTCTGTTCTGAAACCTGCCCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTTCTTCTGAGCGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTGACGCCGCTAACTCAGGGTAACTCCTATCTCTCCACCGGTAACAGAGGGGTACATTATGGGTCCAGGTT CAACATACATTATGGTGCCTTTTAAAGAAATGTTTACTGAGAACTGTACTGTAAACAACATATTTTTGTAGAACATGAGTGAGAGTGTGTGTGTGTGGCGCGCGGCACGGCATGGCACTGAGGGGATTGCAATGGGJG/AJACAGGATAAAAAGGTATAAAAACCTTGGTCCGAAATCTTTGCTTATTAAACCTTGGCCCTGCTCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21966	26 T G ---				TATACTGGTTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGCTGAGATTTTAGTGACCCATCACTGAGTAGTGATACATTGTACCAACTGTAGGCTTTTATCCCTTACCCTACCTTCCACCCCTCCCCATTTTGAGTCTJG/CJCATAGTCCATTATATCACTCTGTATGCCTTTGCATACCCATAGCTTAACTCCCC
WI-21139a	165 T C ---				GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTGCTCTCTCTGTGAAATGGGTACAA TGTGGGTACGACGTAAGGAACTAATACATJ/CJGTACAGCACTTCAGCACAAAGCCCTGGGCACACAGCACTGCATGGAAATACACAGGTAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCGTGTGGTTGCTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA AATTTGTCTCTTCAGTTTTTCATTAAAGTAAATTCATAAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAJG/JTJATTAAATTAATTGCATATTTTGGGCTACTCT
WI-20317b	217 G T ---				CAGGACTTGGTTTGTGCTGCCCACTGCACATAAATGTCCTTTTTTGTGTGAGTTATTGGTTGTGTGCGTTTTCTCTTTTGCAATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGG GTACACGGGGCGTCCGCTCAGTTCGCCGCGAAGGACGTATG/AJCTGAAGTGGGACGAGTCTACTCCTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-22082e	179 G A ---				

WI-22082b	67 C T ---	---	---	CAGGACTTGGTTGCTGCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATTGTTGTGTG[C /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGTACACGGGGCGCTCAGTTCGCCGGAAGGACGTTATCGCTGAACCTGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTGTGCTCAACCTCT
WI-20993	139 A G ---	---	---	AACACAACTCCATGCTTTCAAGATTCACACCCAGATACTAAGACATATTAATAATTTACAGCAAT TAAACAGTGTAGTTGGTACATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACAGATTTGCAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGTCTTCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	---	AAGCGATTTTATTAAATTTGATTTGGACATAGTGTAGGTCAAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTACTTCAAAAGGTTAGTCATATTCCTCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	---	AAGCGATTTTATTAAATTTGATTTGGACATAGTGTAGGTCAAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGTTAGTCATATTCCTCAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---	---	---	CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTGCTTTTACTATCCTT[G/C]CCCCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTCTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTTAAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	---	TGACAGATCACACCACATTTGTTTGTAACTTTTCTCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACACIAGAGAGGCAAGTACAAAAATGTAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAVAGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAGATTCTAT TTCTCTTTGTGTACAAAGGATTCAAAATATTTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CTC[G/C]AATACACACCAAAGCCAAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	---	AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAAATATCTGCTAGTGGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGTTATAGGATGGGCAAT

WI- 21079a	50 G A ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCACAACTGTG[A]CGCAAAATCAAGT TGTTTTAATACCAGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT[G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTACTACATTTTCAAAATATAAATAATTTGGTTGCAAAATTCAGNAAGGGCA TTAACCAACATGGGACTGATCCTGGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGCTCTGCTATTTTCCCCAAAGAGGACTCGGAAGATGTTGATTCAGGGGCAGAGT GAGGGGCAGAC[A]G/GGATGAGGCTCTTCTGTAAAGTCCACAGAGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGGAGCTCACCCAGAGAGGCTCACTGCATTGACCCACACCCCACTCACCC CAGCACACAGGCACACGAGGGGCACACGACACACGNTGCACTCAACCACGC
WI- 18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAACATCTTTCAGCAGCTCAGC[G]TGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI- 18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAACATCTTTCAGCAG[G]CJCTCAGCCGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI- 19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCAGGNCCTCTGGCCCCAATTCCTGGTTCTCCCCAAG CCCATGCTTCTTCCACTTCTCACAACTTTACTTCTCTGACCCCTCACCACCCCAAAAT[A]G JCTTTTAACTTCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI- 21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACCCAGCCCTGGCCCTG[C]TJAGCTGCATGCCACCCCTC ATATCCCACCCCATCCCAGCCTCCTGCCCCGACACCCCCAGGCTCCCTGCTGTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAAACCCACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C]GJCTGCATCAGTAT CTCCCATCCCACATAATTTCTGTTTGAATTTGCCATTCAACCCATAAATGGTGGGATCTACCTCCCCCT CCTTGCAAAATTTAGCTGGNCCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI- 19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG[C]TJACAGCATTTATTTCCCTCTTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTCTGGCCACAGTCGTAACTATTGC

WI-19891c	172 C G ---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCTCCCCCCCCG ACTCCTCTGCTCGGGAACGTGGCTTTGNCCTCCAGACACAGTGTACAGTCCAGCTCTCCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/C/GCTCTCCGGGGCTGGGGCGTGTCTGT CAGGACGCGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---			GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCAGGGGTGTACATTACCCCTTAGGCTGACCAT TCCCTTGGGGGG[C/T]GCAAACTGCTTTGAGGAAATNCCCCAGGAGGAATAAACTAGAAAGACGC ACCTGCTATTTACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAGCTTGGCCGCTGTGA GTGCCCCAGGTAAAGTCTCTCTCTGTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---			AGCCATACAAATGCATTGCAAGAAACAAGCAGCTGTACAGGAGTGGGACGCG[G/A]TCAGTGTACAAT ACATTTCATGTCAGGATAAGGAGCA[T/G]ACACAGGATTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTTCCCCCGCAGAGGGCTTGGGAGGCGGGGGTGGTGGAA
WI-20270a	53 G A ---			AGCCATACAAATGCATTGCAAGAAACAAGCAGCTGTACAGGAGTGGGACGCG[G/A]TCAGTGTAC AATACATTTCATGTCAGGATAAGGAGCATAACACAGGATTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTTCCCCCGCAGAGGGCTTGGGAGGCGGGGGTGGTGGAA
WI-20622	130 T C ---			CCACTTTCAATATTTAGAAAATGCTCAGCAGCAAAATATGAAAAGCTTCAACACTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTTATTCATATACATCTTTAATGACATCATTTGCCAATACATA CAATATTTCTNTAACITTTATTTTACAAATAGCCAACATCTGTCATGCAG
WI-20768b	190 C T ---			TTCCCACTCAAAACTCCCAACCCCAACCTTCTCGAAGGCGGGCTAACAGGACCTCTGCTGCCTGC TCAGGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCAITCTGTATATCACCACTCTA CAGGAGGCTCTATTTCTGGGCGACCCAGAGNTCAGCACACATACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTCG
WI-20768a	71 C T ---			TTCCCACTCAAAACTCCCAACCCCAACCTTCTCGAAGGCGGGCTAACAGGACCTCTGCTGCCTGC TCAIC/TGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCAITCTGTATATCACCACT CTACAGGAGGCTATTTCTGGGCGACCCAGAGNTCAGCACACATACTGCTGGGACCAAGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTCG
WI-21909	153 A T ---			TGTTTGGCTTTGGCCAGGTACTCTACTGCTTTACATAAAATATCTCATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGTTGGTCATCTTTAAAGAAA TGCTTAACATACCAAAG[A/T]AGTGGGAATCAATAGAAATAAATAATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATATTTCTATGTATGAAAG

WI-22202	128	A G ---	---	TGTTGCTTTGGTTGTTTCTTGAAACATATTGGAACACTTGTTTTTCATAAGCTGTCTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTTAAATAGGTCATTATGAATCTGAATTTCTA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTTGGCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70	C T ---	---	CCAAGGATGAAATTTCCACATTTATTTNCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AA[CT]GAGCGAGGAATGGGCATGGCGTGGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGTGGAGACAAAGGTT
WI-22283	109	T C ---	---	GGGGAGGCATCATAGAAAAAACCCCTCAGCCAGAGAAGTTAGGACATTGTGATCTCAGGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTG[T/C]TTCATTTGCAAAATAAAAACCCA GACCGGGTCATCTTTCAAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAAATGATGCAAAAG
WI-22290a	136	C T ---	---	GACGTATCTCTGAGGGCTCTGCCAGGTGATTAGGTGAAGAGAGGTTTTATGGGCTCTTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTAGTGGGATCTGGGGGGTGCAGGACCTTGTCTTT [C/TT]TCCAAATCTCCTCTTAGCCAGAACITTCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATCCAGACCCCTCCAG
WI-22292	53	A G ---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATGCTCAGTACCAAG[A/G]GTTTGAGTAC GGTGCTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186	C T ---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGGCAGCTGGGGCTAAGGCATATTTAAACAAGGCTCCAAAGGACCCCTT TCACTTGGTCTAGCATCCAGCCTCTCTCAGCAAGGCAGGATTGTGGT[C/TT]CCTTGTGTTTTCTG AACAGGGCCAGGGCAGCAAGGCATGCCATCACTGCAGCACTCAACCT
WI-22395b	127	A G ---	---	GCGTTCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTCTTGAATATTTT GTAGGGATGGATGAATGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAATTA/GJAAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGTAAAGTCCCAAG CTCCT
WI-22405	90	A C ---	---	TTTATGGCTCTGAGTGCCCTTACCCAGCTACACTTTACCTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAAACACTGCTGA AATGTGGCAAGGTTCTCAGTG
WI-22419b	67	T C ---	---	CCCTTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNTCGCCTTCCAGGCACAGCCAGTGC[T [C]CTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59	T C ---	---	ATTTTCCCTTCTGTGTTTCGTATTTCCCTTTTTTGTCAAGTAAATNAGCAATACACTGAT[C/JTGGAA ATCTGCATGATTAAATAACATTAAACAAGTTCTATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTTAACCGAATGCAAAATAGGTATCCCTCAAAATTTGCACATTCTCTCTCTAGTT

WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATGATCTTAGTTAACAGTCTTGAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTCTCAGTCACT GCTCTCCACAGCTGATTG G CAGACATTGCCTGTGCTTCTTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATGATCTTAGTTAACAGTCTTGAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTCTCAGTCACT T C GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTGAGTCCCCAGTCGAGGGTGCAATCTTCTTATCTTGTGTTAAGCCACTTGGGTAA AC TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGGAATACAGTAC TTCCTTT T C GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCCAGAGGGCTTTATTTCAGCCACTCAGGAOCTGGCTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCC A G CCCCACAGGTTCTCTGTT TCCAAAGTCTGATGGATTACAGGCAAGACCTTCACACATTCACCCACTACTGCTGGAGAGGGTCTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTCTTCC A G C G T GTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTCACAACATTTGACTATACAGAG TCTTCAATTCACAAAACAGTTAATAGTAACCTGGTGGCACATACAACTGCAATTTGAATACTCTGTAT TATTCAGTAACTAAA T C AGGNTCCTGCAATCTCTTCACA
WI-22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCA T TCTGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTCATTCAC T G ATAGTGGTTATTATGGGGTCTCTGCTCCTGCTGTGTTATG C T GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCA T TCTGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTCATTCAC T G ATAGTGGTTATTATGGGGTCTCTGCTCCTGCTGTGTTATG C T GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCACACCTCCAGGCCACCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCCAGCAAGTGGA GCCACAGAGGTTTGTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCAACCTG G C AGTGTCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGCTGGAGGTGAGGAAGAGGT

UTR-04932-2a	149	C T ---			GCAGCCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTACGTGGCCCGAGTAGCGACCGCTGGCCCCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTG/C/TJTGGAATCCAGCGAGGGATGAGGCCAGCCCCAGAACCTGGAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTCTCTGGAGGTGAGGAAGGAGT
stFIBBb	412	G C ---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATCTCCAGATGACGCCAGGAGCCTCTCTGA AGGACCATCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C ---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATCTCCAGATGACGCCAGGAGCCTCTCTGA AGGACCATCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stGLV2	61	T C ---			GTCACAAGAGGCGAGCGCTCTGGGACGTCTCCACCATGGCTGGCTCTGCTCTCACTCACT/CJCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCCTGGTC TCCTGCTCTCAGGCTCACGGGGCCAGCACTGACTACTGGCATGT
stSG1001	70	T C ---			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTGGGAT TAT/C/JAGGCATGAGCCCCCAGACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG1001	33	G A ---			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGC/G/AJATCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGCATGAGCCCCCAGACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG1002	63	A T ---			TAATGATAATTAGGGCATCTTCCACACGAGATGACACAATTGACCCCAATATCATTTGAGGC[AT] AACAGTTGGGCTGTTTCCAGTAGTATGACAGTGA
stSG1009	36	G C ---			GTGGAGAAAGATCGTCTTTCCTCCCTCCCATGACC[G/C]GGCTTCCCGGGGCACTGTGCGTTTCC ACCCGAGACGGCCTTGTAGGGACCCACTGCCCACTCCGCTGTGCGCTGGGTTCCGCTCTCTAG GGCTCGAGTGTTTAAG
stSG1011	107	C A ---			TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGG[C/A]CTCAGCCCTCAGTTCTCTTCAATTC ACCAGCGGTGCTGTTTGGTTTTCCTCCAGTGAG
stSG1012	89	T C ---			TAGTAGGTAAGAAAGCAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGCAGACTATGC CGTGTTCACGAACACTTTAATAT/CJGTGTTGTATCTGATTTTATCTCTGCTTACAAATG
stSG1017	42	C T ---			TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAGTCCG[C/T]GGGAGGAGAGTGAACAGGAA TCGATTCTTTGTCTTTAACTGCCCTTAGTAGGAGATGTTAAAATACITGGC

stSG1019 3	136 GA ---	---	GGAACAATACCTAAGGACAAAATACTATTATAAAAAAAGTCTCTAGTGTATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTACTTG[A]TTTGAAACTGAGATTTAAGTTTGCAAACT
stSG1020 2c	143 GT ---	---	AAGCTAACTTAGGTGAATGTGGCCACTCAAAGGTCTTTCCGAGGGAAGCTCAGTCCTGGCTTGGGAGAGTCAGCCTTGGTCACCTCATACGGGCTCCAAGCTAAGCGTCAAGGAAGCAGTCCCAGCTCTCTCGCTGTCA[G]JCAAGACACAAAGGAGATGCCACTGCTGCCCTTTCTTCTGTACTTTCT
stSG1020 9b	75 AG ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCATAATAAACTAATTCCTCTAAGATCCCACCTTTATTTTTA[G]CTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1020 9a	34 CT ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAATTCCTCTAAGATCCCACCTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACAT/CJGTGAATATTTAAAGAAGTTATATTTGTTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATCTGA
stSG1025 2	108 AC ---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCACCTAAGAGATTTCTTTCTCTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAATTAAGAAGGCACATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAATCTGTACTTTAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG[A/C]ATTTTAAAGAACTGAGTTATTGGAC
EST11023 1	166 TA ---	---	TTTTTTGTTAAACCAACCCCTGAAAGTTTCCACATGTGAATATAGATACAACAGTGAACAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACACAGCAGGCAATTAGTCAATTAAAAAATAGTACATGTTAT/AJGTGTAATAAAATTTAAATTTACAAAGGCTTTTCCACTCGTGGATTTGATTCCTTTTGGAGGGAGTAACTCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACCTACAATAATACCATCAGACATTGAAAACCTAAGGCCATTCTGTGA[G/C]TTATTTTAAACCTGGTGTTTGCACATAATGATCTTAAAAAATAATGAATTTACCAAAACCAAGATTCTCTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	TGCAATTGTGAGAAGGCAGAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGATGTGAGGTGCGCAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA[C/A]CCCTTCCTCAGGGTGTGGAG
EST22555 7	60 GA ---	---	TCAAAGCATGTGTAAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTGCACACTGGAAGGT[G/A]AAACCTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTAOCCTGGCACCCTCCCAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/TT]GACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGCTCACTCA/A GTTGGTTTCTAGCCTCACTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAAAGTCACTCTCCA GAGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGATCATGGGGCAAAAGTC/A/GCTATGG GGCCAGACTGAGGTTGGACACACAAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGGCAT
EST36745 3	56 A G ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGA ATTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG T/A/TJTTTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGA ATTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	TATCGTGGGAAGTTCCAAACCTCATCTTATGCTGCTTTTCTACTTGCTAATATTGGATGCTCTTGCCA GGCTC[C/TT]TAAATTGTCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	GAAATAAACTAAACTGCAAGCAAAATCACTGTTAATAAGAAATTGTTCTTCTGTTT[C/G]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCCAATGAGGTCCTCAGAATCGGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1026 6	55 T C ---	---	GTATAATTGAGCATAAGCCAAAGCCTTTTAAATAACCAATCACTATCATTTTATGAAATCTTTACA AGAT/GJAAGCACAGTAGTACAAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028 2	70 T G ---	---	CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTCAAGCCAGTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTATGATATGCAATAACAGCAAAATAATTTTTCACCT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCCCAGAAAATGAGAAAAGGATACAAAACCTTTTGTATAAAAAAGGTA AGAATTTCGTGIGTG
stSG1031 0	128 C A ---	---	

stSG1033 1b	116 T C ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAAGAAAGGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACACCAACACCTCCATTCGCAATTCCTCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCACTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAAGAAAGGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACACCAATTCACCTCCATGCATTTCCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCACTGA CTTAGGACCTCC
stSG1243 b	225 G A ---			ATTGGCAAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACCTTCGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCCAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTC[G/A]AAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTTGTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTTGTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1345 b	60 G A ---			TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGAGGGTTGAGAGCGAGAGCGAGTTATTT TGGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGTATTTT[G/G]TCAATCATTAAGAA GACAAAGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG
stSG1385 b	117 T G ---			TCGTCTCCTTTCCAGTGTCTGCCAGAAGCATCCCATGATGTTGTGACCCGACACGACCTTTGTGTCT TT[C/G]CTTTGAGCACTTGCCACTCTGGCTGGTGTCTGCTGCCACTGAITGTACTGTCTTGTGCCCC GATCTGGTTCCAGACAAGGCTGATTTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTTGGCTTCTGTCTCTCTCATTCAGTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCACTGCTCTCTCAGCTTGGAATCCAGCAGCAAGAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---			CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCAATGTTAGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---			CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCAAGTTTCJTAAATCAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAATGCTTCCCTTAGTTCGAGATGGTA
stSG1483	44 T C ---			CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAAGGCCAAACCCAGTGGCA [C/G]AATGTGGAGGATGTCTGTTCAGCTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAAAGAGGAA AATGCCTGA
stSG1696	67 C G ---			

stSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC[AG]AAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGATTTTCGATACCTTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAGCGGTTTATATGGCAGATGAGCTGCTACAATCTGTTGTGTGCT [C]TGGCGGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGGAGTGGAAGACCA
stSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA[C]TCTACATTCCTCCAGTATAATA GGAAGCTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTTCGGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCCTGTATGATG[T/C]TTTATATTTATGTAT AATGTCTTACCTGATGATACCCACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTTCTGCCTCCTGCTTCCAGTACTACCCGCTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAG[G]TAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGTCTAACTGTGTAGGCGAGGTATCAGAAGGGCAG[A] C]CTGTCAGGAACTCTGCCAAGCACTGGGCTGCTCTCAGGCAGAAITTCCTCCT
stSG2306	67 A G ---	---	GTCTCAGCGTAGAGGTCAGTGGTATAAACAACAGTAGCTATATGATATTTGGGAATATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT/GTTCAGTGGAGGGGCTGTGGGAGGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTGCTTGAAGTGCAGAAAGTAACTGCTGTCAC[T/C] GTTCTCAGAGTCACCATTAACGGTGAAGTGTCTATTTCTGGCTGTCTTCTTATCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAAGCCGCAACCGAGTGGTCCACTCAAAAAAGAGATTCTGATTCTACCTCAAAATG CAGAAACCA[C]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGATTTCCACAATAACAAAGTCATGTATAGAGAAATGTGAAATGATACITGAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTAGTACTGGTTAAATATGCAAGCAGCTAAAG GAATA[T/C]TACACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGAAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCAATCCCAAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATC CCGGCCACAGATTAATATT
b			

stSG2577							AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTGCAATCCAGTTGGTCCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAAGCTGTGAAAGCTATGAAACAATCCGGCCAGATTAAATTATT
a	121	C T	---			---	ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTGTCCGGCCCC[G/A]AGTCACTCAGCGTTTGGGGAAATAAACCACTGGTCCAGAGCAGAGGAGGCTACTTGAGCCGGACACCA
stSG2700	58	G A	---			---	AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTTATATTAATTTGCAAAATGCTATAATTTAATACTTATATCCAAATGCTTGCATAATCA[T/G]TTTTTTTAACTCTGGGTGTTGAAAGAAC
stSG2724	101	T G	---			---	GTGGCCGATCTTTACTTTCCAGAAAGGGGTAAATAAAAACCTGTAGAAAGTCTCGAATATG[G/A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCAAAAAATATCCACTAATCCCGAATATAGTAACCTGCTTGCCGAATG
stSG2776	65	G A	---			---	AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTCATTATCTCTGAACGGTAAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA
stSG2791	109	G T	---			---	AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791	100	A G	---			---	AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTCATTATCTCTGAACGGTAAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA
a						---	AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
							CCGCAATTTTCAACACACATTCTATGAAACTAAGGGTGGATCATGTACAAACACAAAAACAAGCTCCCTCCCTCCAAAAACAAC[C/T]GAACAAAAATAAAGAAAGAAAAACCCATGAAATGCCAGGTTTA
stSG2826	85	C T	---			---	ATTTTTTTCC
stSG2850	88	G A	---			---	ATGGGTGCATTGTAAAGGCAAAATTAATACTTTTTCAGGCAGGGGCTGGCAAAATTTAATGAGCTGATGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG3031	71	T C	---			---	ATACTCAGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCTGCAATTTTCTGTGGTGCAGGAAA[T/C]GCCCTTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A	---			---	GTCCCAACTCCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAACTGTGATTGAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAAGGCAAAACTGGCTGAGGC
							CAGCATCTCCAGAACATTCTAGAACTGAACCATCTTGTACATATTGAAAAACAAAGCCAAAGTTCCAAATCCAAAAATAAATAAATGAACGTGC[T/G]GATAAACATTCTTCTATGGTTCCAGCCCCCTACTTT
stSG3092	94	T G	---			---	AGTT
stSG3230	95	A G	---			---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTGCATCTTTAGTCAATTTGTCAGTGGAGTC[A/G]GTGGGTGCTAAGTGTCTGAACTGAAGTAG
							ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCCCAGGTATGTAGAGGCCAGTGGGGGTGGCCACTTGGTGTCTTACCACCCCTGCCATCCAGTCTGC
stSG3245	160	G C	---			---	GCCCCAGTACCTACCTGGGAGGTT[G/C]TGTACTGGCTTAAGTACTTCATGCTTTAT

stSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/CJGCATTGTGAATAGTTTCTCAG TTTTCAATTATGAAAGATGATGATTTTCAGCCACATTCAGTGTATGTTTCTAAATACACAATCGAC AGGACTGTCTGTTTCAGTACAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAA
stSG3269 b	141 C T ---			TGTACTTACTGTGTCATCCTATCCATTCCCTGAGCCTGGAGTCTCTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TJTGATATCCCAAGTCCCTGACACATTTTCTTAAGAACT
stSG3269 a	24 A G ---			TGTACTTACTGTGTCATCCTATCC/CJ/TJTCCTTCCCTGAGCCTGGAGTCTCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3284	130 C T ---			TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/TJ TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTGTTTGTATCTACCC
stSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAACTGCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA/J/TJACAAATCAAAATAGCATTTTCTTAACCTCAA
stSG3323	26 C A ---			TAAATGTCATATCTTTAGCTCCTACT/C/AJCCAGTGTATCCATTTCCCAAGCCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGTCCCTGGACATTTGATATAAATGGAGTGTCTGTATCATGTTCCGACTTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTCTTATCCCTTTAA
stSG3369	69 C T ---			GATCCCCAGTATTATTTCTAAATTTGAACCTTGTGTTGTGGAAATAAAAAATCTGAGGACCCTCAGAG GG/C/TJATAAGGGGAACCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3398	125 G T ---			CAAGACTGTAAAGACGTAGGCCCTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACTTTGTAGC/G/TJCTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3416 a	43 A G ---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/JGJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCAACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173 T A ---			GTAAGACAAAGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGCCGACTTTTAAACTGAAT GTTGAAATCATCTGCTCTTGTCTGGTAACTGA/J/CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCCTTATCTGTAAACAAATGGACAAACAGAACTTTTCCCTTCCCTC
stSG3436	88 T A ---			GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTCAAGGTGATGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGGCCCTT/AJGAAATAGCTTACTCTGTTTTCCTATC

stSG3463	103	C T ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTAC[C]/TJTGGAACAAACCTTGCTTGACTATATTA CTGA
stSG3491	71	G A ---	---	CAAGATACCTCATTGTCTCTAAGTAGTGCAGTCTGGCAATATTTCTACGAACAAGGACGATTG AAG[A/GA]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTCTAATCTTTACTGGCACCTGTGGATTCTATTAACACTCATTTACTATTTTCTGTGATG ACAGAAAAAAGTTAAC
stSG3523	33	C T ---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTT[A/C]/TJGCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213	A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACAGAGCTGTACAAACCCAAATACAGAATGGCTTC TGTGATACCTGGCCTTGTGAAACGCACTCTCAGTCTCATTTCTATTGTTTATATGTTTAAATGAGCTTG TGCACCATTA[G/A]/GTTCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112	G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATCGTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]/TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586	60	G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G/C]ACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGTGTGTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCATTGCACTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101	T C ---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGA[T/C]/CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590	70	A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTTCTAAAAA AAA[A/T]TCTCTGATGCTCTTGACCTGTAGGAACACATTCAGTTTCTACACT
stSG3619	78	A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATACGCT TCTGTCAATTT[A/C]AACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40	T C ---	---	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTTATGAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA GTGCTCTACTA
stSG3646	70	G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCAATTTGGCAAGAATATATGATGATAACAATA/GJ/TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTTGTGA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCAATTTGGCAAGAATATATG/JT/GATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTTGTGA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCTACGAGGC/JCTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCTCC/JT/CTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145 G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCAAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/GJ/AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCAAGGTTG/JCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATAACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCTGCTGGATCCCAACTGGAGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/JT/ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATTACCAGCCCAACAGCAACAGCCCC/JA/JAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAATCCACAGGAACAATCTATGTTTCATACCTTTTGAAGAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC/JG/JTT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTTAT/J/AAAAGTTCCCTAAGA CACTGAGGGCATAAACCAACAAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---	---	GACAAGAGGAAGAGATGCGCCAGAGAACAGGGCTGGGCAGCTGGGGTCCCTGAGTGCCAGGGCGC CACCACAGTCTCTGTGGGTCAAGGCCCTCTCTGGGGAGCAGGCTA/GC/JG/CACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT

siSG3880 a	36 G C ---			GACAAGAGGGAAGAGATGGCCAGAGACCAGGGCTG[C]GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGCTAGGGCAGGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCATTTCTGCCCT
siSG3895	44 A G ---			AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTGT[G]G/TTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGAACAAGATGCTGATTCGTCAACTG AAAAT
siSG3902	104 T C ---			TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGAACTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAAGTCTTCTTTCT[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTGTCTGGACAAT
siSG3935	50 G A ---			GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTACAACTTCCTGGACGT
siSG40	25 A G ---			GAGGAAGAGGTTGAAGAAGTGTGA[G/G]AAATATATTTAAGATTTCCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAATAAACCCCTTGTGTATGTATCA CCCAA
siSG4009	32 A G ---			GTGTGGGCTGTCTGATGATGAATGGCGCGCT[C]G/TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGCTGAACCATATCTGAAGGTTTCCCACTGCTTACA
siSG4033	123 T C ---			AGAAAGCTTGGGACAATGGCAGTGCCTTTCTGAGTAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGACTTTT[C]TGTGAAC AGGTGGGCAACAC
siSG4038 a	29 G A ---			GCTGAGAGCACGTGTACAGCCACGCCCTGT[G/A]JCGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTCAGGCTCCCGGAGAGCACCTGAGGGTCCATCACT
siSG406	53 T C ---			ACTGTGGTTCAACAGTATTGCGTTGTGACACTAGGAAAGCTAAACGAACAAAAT[C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCTTACAAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55 G T ---			ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGCTGCTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4095 a	27 A C ---			ATCTGGGCTGAATTAGTCAAGCAGGTC[C]GATACTATTGCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4120	65 G A ---			TGCATGTTCCACATCTTTTCAACAGCAAAATGTAATAATAAAGTTACGTACTTATGGATAATCAC[G/ A]CTTTTTCCCTCAGAGAGCCACAGTTAAACAGTTCCAGCACACCAATTAATCCACCGAGCT

siSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCCTTTGTGTACATTTCTT/GTATATTTT TACTTCTCTGAAATGCCACATAATTTGCAATAATGATTCACTCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAATGTTCCAGAGGG
siSG4209 b	128 G A ---	---	CACGAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGCAACGAAGCCACCCCGAACCTTGACAGGCGCCACTCCCTC[G/A]GC AGGGGACCACGGAGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---	---	CACGAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A]CAGGGCCGGCCACTCCAGCAACGAAGCCACCCCGAACCTTGACAGGCGCCACTCCCTCGGC AGGGGACCACGGAGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACCAAGAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGG GCTATGCTCTGACAAGAGGATGAGCGAGGGCGGGGCTGCTCTCTCCAGGGGACAGCGTGAC TGGGGGACCACATGGCCGAAGAGAGGATGACCGGTCATG
siSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAATAAATT/G]AGCTTCTGAGTAGTTGTTCCAGTTTCAACCAACATTTTG
siSG4331 b	71 T G ---	---	CTCACAAGGCCAACACAGAAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC AGAGT/G]TTTTCAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCCTCGCCCTTGATCTGTTTGAGSGGTGTC
siSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCAATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG AAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACTTCACTTCACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGGAGG
siSG4361 a	24 T C ---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCAATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACTTCACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGGAGG
siSG4376	73 A G ---	---	TTTCACTGCTACTGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTCGAAGTCTTCTCCAAAGGGGAG AACAG/G]CTGGAACCTCGGCTCTGCAAGAGCCATCTTTCCAAAGCCATTTCTTCTCAGCTGC
siSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTTT/C]TCAGTCTTGTAGT ATCCACAGTAGTGTCTGTCTCCATGTACAAGTGTCTGTCCAGAACACCCATTAATTCATGCC ACCAATGGTCTGCTATGTCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCCG[G]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGACGAGGGTGGCTTGT
siSG4410	79 A G ---	---	CAGCTGGGT

stSG443	65	C T	---			AGCAGATCAGTCAGCCACTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/TGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGGAGGAGGAGGGAATAGGCAC
stSG4430	54	A G	---			AAATGGAATCTATCCTGGCTGCTCTCTCAGGTC
a						ATGCACATTAAATGAATGGCCTAACTACTGGAACTTTAGTAGTTCTATAAGGTJAG/JATTAAACATA
stSG4448	99	G A	---			GGTAGGATCCAGTTTCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
stSG4449	92	T C	---			CCTCCCTTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCTCCGCCACCCAGGCTCT
						CGCCTAGCCCTGCCCTCTGGGGTCACTGC/G/ATJGGGTTAGGCCCCCAAAAA
						ATTAGCCATTGATCTTGAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACTTTGGACAACITTAACCTTAI/C/JTAGTGACATTGCTGTCTAATAATCAAAATACCTTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A	---			CAGACATGAGGGATGCCCTGTCTCTCTGGGACAGAGCCCTCA/C/AGATGATGTCCATGTTTGTGT
stSG4475	21	A C	---			GAATGAACTCAACACTCTTCAGTTTTAGAGTCATTTCTGGTATCGAGCGCACACCGAGGAG
stSG4477	32	A G	---			CACACCTGCTTCCAAGGCTGCTGCCCTCTGCACACAGT
						ACATGTCAATTTCTGACCAGG/A/C/JATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAACTGGACTTTTGTTTCTTTTACTGTAGCACCCAGGTTTCATG
						GTAACATCTGGGGTGGGGTGAGACAACA/C/AG/JATGAACCAATAATTAATTACAATTATACATT
						TCAAGGAGACTTTTAATCTAGGTTAATGTAAACGCGAGCCATCAATGTTTGTAGGAAAAGGAGA
						TGAAGTCTGCTCTGGGCAACGTTTGGCCTCATTCAGTCAGACTTGGC
						TGAACAGAGCTGGTGGGAGCTGCAGGCGGGGAGGCTGGGGCCAGATGAGCGCGCGGGA
stSG4531	79	C T	---			CAGCAGCGTGG/C/JGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTTGGACTCGATCT
stSG4550	86	G A	---			GATTCTCATTGACAGGGGAGACGCTGTGTCATCAA
b						TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGGCTTGATGAGGACAGAGTCTATT
stSG4550	85	C G	---			AAAAGAGACAGTGGGCACC/C/A/CAATTGGAGGGGAAGCGGGGCGAGGGTTTATAGAGAAC
a						TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGGCTTGATGAGGACAGAGTCTATT
stSG4590	47	A G	---			AAAAGAGACAGTGGGCACC/C/G/GCAATTGGAGGGGAAGCGGGGCGAGGGTTTATAGAGAAC
						AATCAGGCACAAGCTCGGGAGAGAAGCCAAAGCTCTTCGCAC/A/G/JATGGGAGGGAGACAC
						CATTGAAAAGGCATGCTCTTCTTCATGCAAGCGAGGCGCTGGCTCCACAGGCATGGTCTCCTTG
						AATCTGTATCACCCAGCGTGG/J/C/CAATGTACTAGTACTTCCACAGGGATTTTATACTATTC
stSG4623	22	T C	---			CTATAAGGTTTATCATGAATAAAAAAGCTCACAACTCTTTTCAGCCATTGCAGATTCACATTTATCT
						TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A C	---			TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTGTAGTTTATGTTTTCAGATTTAAAG
						GTATTTCTTTCTTAGCTTCTAAATTTTGTAGTCAT/A/C/JATCAGAAAGCTTCCCTACTCCAAAGGTGA
						GAAAGGA

stSG4850 a	38 C T ---			GGAATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC/TGTCAC TTGCAGGCCACGTCAGGAG AGCCAGCGGTGCCCTGTGCGGAGGTTTCCAAAGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGAATCTTGGGTCC
stSG4879	86 A G ---			AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTTCTGTGAGGTCTGCTTTGCAGAATGGCCTG CCCTGGGACTGGAGCAG/AG/CTTGGGTGAGCTCTAGGTGGAGGGTGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---			ACTGGACTGGCTCGCTTGTGAGCCGGCTGAGCGGCTGGGACTCGGCTGACCACTCGCTCTTCAG AGACTGCCCGCCGGTGACCACGACTACGCTCTGCC/G/AGTGGGAAAGCAGAAGCAGGACC
stSG4896	112 C T ---			AAACAAATCAACCCAAATCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGAGCTGAGGAGTGTGGGGCTGGGCACTTTCTCTCAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---			ACAGTGCCGATGGTTACACAAATG/AJTTGTAATGTAATTAATCCCACTTACGAATGATTAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGGGTGCAGGGGTGCTGTTTCTGGTCC
stSG4950	24 A G ---			TCATGACTCCCAAGGAAAGGTCCT/AGTCTTAGCTTCCTCCCTACCTTCCCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTCAAGG
stSG4957	136 G A ---			AGATACGGGCAAAACACTGGGATGGCTTCCTGACAACTTAAGAGGCTCCGAGTTATATTCTGGTT GGGAAACTGACCCAGCCCTTATTCCTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC/G/AGTGACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 C T ---			GAAGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGT/AGT/AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---			ACTGTGCCCTCTCAGCAGATTCAGGGTGTGTCAGGGCTGTTACCACAACTCAGTAGGAGTCAA GGGCT/AGT/ATCCCCCGAGCTAGACAGCCTGGGTTTGAATCTCAACTCTCCCTTTCTTGCTGTGC AACCTTG
stSG4997	22 T C ---			CAAAGGAGTAGGAGCCCAA/T/CJTTTAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T ---			ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAAACA/C/TJATGCCATGCGGGAAATAAATGCTT ATCCAGTGAGCGCTCCCTGATGCATTGAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---			GCTCTGTCAGCAAAATCTCCAGGACAGAACCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC/G/ATAGTTCAGGCAATTAAGAATAT GCAOCCAGAGAAATTTCTGTGAAAAACATTTTGCTCTTTGGCCTGGTGTGGACAGAAAGGTGGCCAA ATGGATTGATGAGCAGACATG

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ESTD-C7	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAACTCCTGCTGGA
ESTD-CB22	--	--	--	---	---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTCCCAACCATAGGGGGATACAAAAGAC AGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGGAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCTCTTCCCGGCCCTTCTCTCACACAC
ESTD-CB23	--	--	--	---	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTTTGGAGCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACCAAGTGGAGCTGAGTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACAGACAGACCCGACCCCTCAAGGAG
ESTD-CB25	--	--	--	---	---	---	GTTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTCGCCGTG TCTGCTCTGAAACAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCACTG TGCACAGGTACCTACATGCTCTGTTCTTGTCACAGAGTCTTACCAGCAAGGGTCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGTAACCAATAAAAAAT TGTTGTTGGGCTGGTTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAATGCTGCT TTCTCTGTTTCATCCTGATGGAAGTCTCAACACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	---	---	---	AGAAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCCTGTCACTTTCAGGGTGTTCAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	---	---	---	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAAAATCCATCAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAAC TGGGAGGCCGGGCATAGTCTCATGCCTGTATCCAGCATTTTGAGAGGCTGAGGGGGTGGATCAC TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTGGCTTGGATTTCAGCGGCACAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTCTTCATCCCTGCTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGGAGGCATCGCCAGCTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCGAGCGTGGTCAGGTGACCATCCCGGAGAGAACAGGTCAGGCCGAGAGCATACTCGG TCTCATCATTTGAAGCTGCTCTCAGGGTTCCTTGGCCCTGAGCAGGGCGGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTCCAAATTAATGCAATCTAAATGTCAACTGATTAAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATTGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCCAAGCCCATCTCTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCGGTG GGTTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTGGTTTCAGTTGCACATTTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGAGGAGAAATTGCTTGAACCCA GGAGGAGAGCTTGCAGTGAGCCCAAGATCACACCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCCTGAAATACATAATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACTTATTTATTGGTAAGCCATACATAAATTTCTAAAGCATGTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATCTGTATCTCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACTGACAGGCATTTATGCCACCTGAAATATGGTCAGGTTACAGGTGATTCCC AGAAGTGAACATACTGCTCTCAGAAAGCAGAGTACATGATGTTCTGTTCTGGTCTTCACGATGG CAGGTATGAATATAATAATCTGTCTTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGATTT CTTAAACAATAAATGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTGAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGATTT GCCAATAAGCAGTAATATTTTGAGAGGAATCTTGTTCATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACCTTCTTCTTCTTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGACACCCGAGGGCTCCAGGCTGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCTCCACT TCCATGGGTGTGGGCTGGGCTGAGCTCACTGTCTGGGAGAGAGGAGGTGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCTGTGGTGGGAGGAGCTGCTTCCAGACC TCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAGAGT
ESTD- DRD1	--	--	--	---	---	TCCCAGCCCTATCGGTCAATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTCGAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGCTGGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGCTTTGTGACAGAGGTGCCGGCAGAGGAGTGGAGTGGAGTGGATGCTCTCCAGCACCA GCCAACCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCACTGACTCTCCCGACCCG TCCACCAAGGTCTCCACAGCACTCCCGACAGCCCGCCCAACCCAGAGAGAAATGGGCATGCCAAAG ACCAACCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGACATGGCCAGGATGAGCGCGCAGTAGGAGAGGGGCATAGTAGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCACACAGGTGTAGTTTCAAGTGGCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB82	--	--	--	---	---	TCTTCAGGATCCGATCTGCGCTGTTGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACCAAGCTGG GGTAGGGGGTGGTGGTCACTGCCGGGGCCGGTGCAGACCCACCGGGCTGGGAGGACTTCAACC CGCTCACCTCCGTTTCTGACAGCTCTCCGCATCGTGACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTCTTTAAGTGAAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGTTCTGGCTGTTTGGATTCTCAAGGAGCGAGCATGCTGTGGACACACAC AGACTATTTTAGATTTTCTTTGCTTTTGCCTTTTGCACCAAGGACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCATTTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCCTAGTAGCCCAACTGTGTCATGCACGCTTAACCTCT GCACCAATGGCTCCAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTCTAATTTTTTACAGTTTGAAGTTTATGATTTATGCCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGATGATGTTTAACTCAAACTTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- G2H	--	--	--	---	---	CGCAGACCGGTCA GTGGGGTGGGAGTGTGAGGGAAGGAGGAGGAAC TGGGGTTTAGGGACT TTCCGGGGTACITTC CCGTTCTGTCTTCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGCACCGTGTCTCTGCTGCCCTGTTCAGCTGTCTGCTGCCGACGTGCA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTTATGATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACCTGGCTGG AGCAGGAATGCCAGCGGCCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATCATG AAACCAAGTTTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTCACGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	CTGGGCTGCCCCGAGCAGCTGCTGGCACCTTGACGGCGGCCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGGAAGTTCTCCACTGTTAACCAGTCTATGTTGGCAATGTGGCCTGGGCCACATTCCTGGCCTTG AGGCCCTGAGGACCCCAAGAGGCCCAAGCATCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTC AGATGGAGCTTTCCTTATCCCTGATGATGGATTGGCTTCCTGCTG
ESTD-HT2	--	--	--	---	---	GGGCTAAAATTTCCGAGCAACTTTCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAAGAGCGCGGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGTTCTTGGTGCTTCTATCGGCAAGAAATGCGTACTTATTTGAATAGTAGGTA ACCACACGCCCCAAGAGTCACTGAGACTGGCAGCTCTGACAGCGCGGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACAAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTCTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGGTTTTCTTCCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCCTCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTCT CAGGGCACACATAGCTTAGTGGAGCTC

ESTD- IGHV4-6	--	--	--	--	---	---	---	TTTACTATTTCAATGATACAGAAATTGTGGAGTCACATATATTCTATGAACAAAAATTCAGATTT CAGGTTAAGTAATGTTGCTACATTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	--	---	---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATATTATTATTATTTATTTTTTTG AGATGGAGTCTGGCTGTCAACCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTCAAGCTCTG CCTCCTGGGTCATGCCATTCTCCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	--	--	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCAATTTAAAGTAACGTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCCAAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8	--	--	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCACATTGACACA
ESTD- LF79	--	--	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGAACGTAGCAAACTGCATTGGTATTAGA AAAAATAAAAAATTTCCAATATGTAGTGTGTGTATTACCTGCCTCTGCCATCGCATCATAGCCTGT GGGAACCAAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	--	---	---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	--	--	--	--	---	---	---	TGTCAGTGTCCCTAGGGCACCTCACCACTCCAGCTTCTCAGCTCTGCCCTGCTGCTGCTGCCA AGGTTTTGCTTAATTCATCAATGCTCTCTTCACTCTTAGCAGCTGGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTTAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCTCCCCAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCCCCGAA TCTCAGGAAGTCTCTGCTTCCCAAGGGTTGGTCAAGTGTCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTTCATG
ESTD-NF1	--	--	--	--	---	---	---	ATTATCCAGATGAATTTACAAAATAATACAGATCCCAAGACTGATATGGCTGGT

ESTD-NFKB1	--	--	---	---	---	AACATGGAC TTGTATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAAGAA AAATTTAAAGGGGTAGCTTATATCCACACTGCACACTGCCTAGCCCAAAAGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAAC TTTTGTAGGGGACGAGAAGATCATTTGAAATTTCTGAG AAAAC TTTCTTTAAACCTCACCTTTGTGGGTTT TGGAGAAGGTTATCA
ESTD-NPPA	--	--	---	---	---	TGTCCTTAGGCCAGCCCTGCTTGCTCCCTGGCTGTATCTTCAGTACTGCAAAGAGAACACAGAC AT
ESTD-NRAMP	--	--	---	---	---	GGAGCGAGAGGTGGGAGGGGCTGTCTGCTCCAGGTCOCACAGACCAGAGAAGCGGCCCTCAGTG TATCCCAACCCCAATGTGGCGCTGGGAGATGAAGAGAGTTGATGCAGGT
ESTD-NRAS	--	--	---	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGAACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGTTTTCTTTATGTAGGGTGATATTGGATACTTTTGTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	---	---	---	GTGACCTTCTACITTTAAAAA ACTTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAACA
ESTD-PAI1	--	--	---	---	---	GCCACCACCAACCCACCCAGCACACCTCCAACCTCAGCCAGACAAGGTGTTGACACAAGAGAGCCCC TCAGGGCACAGAGAGAGTCTGGACACGTGGGAGTCAGCCGTGTATCATCGGAGCGCGCGGGCAG ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGCCCAAGTCTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	---	---	---	CTCTTCAGGAACCAACAGTCTCTTACCAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCTAACTGTAAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCAATTAGCTCTGTGAGTGTTTCTTTCACITTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACTTAGGCTTTCTGTATACCCATGCC
ESTD-PBDA	--	--	---	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAAATCTTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGTGGAACATTTGAAAGCCTCGTACC
ESTD-PS-1	--	--	---	---	---	GGGAGTAAACTTGGATTGGGAGATTTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAATAGCCTATTCTGAGCCATATTAATTTGTTGTGCCCTTACATT ATTACTCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCCTTTGGGCTTGTTTT CTACTTGGCCACAGATTATCTTGTA
ESTD-PXIPI	--	--	---	---	---	ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAAGAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAAAATCATGGTCCCTAGAACATTTTGTAAGAGGTTAAGTCTTATGAAATTAATCTT
ESTD-Per/RDS	--	--	---	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCCGAGGAATCTGAGAGCGGAGCAGGGCTGGCTG CTGGAGAAGAGCGTGCCGGAGACCTGGAAAGCGCT

ESTD-FDS	--	--	--	--	---	---	---	---	CCCGAGGAATCTGAGCGGAGCGAGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGGAGACCTGGAAGG CCTTTCTGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTTGGAAGCCGAGGGCGCAGACGCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCCCTCCCTCCCGAACACTGAGAAATAGTGCACCT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCIGAA
ESTD- RYRI	--	--	--	--	---	---	---	---	CTTCGTACCGGAGGTCACGTCTCTCCGCCTCTTCATGGACATATGGATGAGTGTCTGACCATTTCCOC CTGCTGACAGTGTATACCGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTCGCTGGGGCCAGGCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	--	---	---	---	---	TGAACACCTGTGTCCGGAGCCAGTTGTGTTCTCCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCGCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACCTCTTTGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAAGACCCCAACCCCTGCCCTCC CCACCCAGGCCAGTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	--	---	---	---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGCGACACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCCGTGCTTGTGGGATATTTGAAGAGATCTTTGCCAGTCCCAATGTCTTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGGGCCCTTAGATTTAAGTCTTTAATCCATTTTG ATTGTATTTCTGTA
ESTD-TAT	--	--	--	--	---	---	---	---	AAATGGTCAGGACCTGATCCACAAGAGTGTACCAATTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTTCCAGTATGGATGGGATTATGATGGGGGG GAGAAACAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	--	--	--	--	---	---	---	---	TGCGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCCA CACTGGATTGGCCCAACAAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	--	---	---	---	---	TTCTGCATCTCTGCTGGAAGTTAGAAGGAAACAGACACAGACCTGGTCCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAGACCCCCCTCAGATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGTCCTCCAACTTCCAAATCCCCCGCCCGGATGG
ESTD-TYR	--	--	--	--	---	---	---	---	TAGTGAAGTTTTCATCTCTCTGAGCTTCTGGAATTTCTTGTTCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTGTCATAAATATTGATGTCGTAAACAT GGGTGTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD-TYRP1	--	--	---	---	AGTAGGTGAAGCTAACGAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAAGTGTATTTCTTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACCT
ESTD-VB12	--	--	---	---	TCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTACAGACAGCAAGAACACCAGTG ACTCTGAGATGTCACCAGACTGAGAACCCGGTTATATGTACTGGTATCGACAAGACCCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCGACTCTTTGTACGGTCTGAGACCATCTGAGAACGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGA TATCCCAAAGTTGAAATGTCTCAGTTGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAAC TCT
EST71770	--	--	---	---	AGCACCACTCTCAGTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCTCCATGAAGAGACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCACTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
EST52418	--	--	---	---	CAAAATACAGGGTCAACTGCTATGATGTGTTGGAGCCCCAGTCAACCTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGAGTTGGGAGTAGCGGGCTGCAGGCATACACTAAAGTGAAGTGTGAGTGTTG
EST13586	--	--	---	---	CCCACTCTATTGCCCCAGCCCCAGGGACAGAGTATCCTTGAAGTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCTCCAGCCAGACCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCTGCTGCTGCTGCCCCG GTCACTC
EST51976	--	--	---	---	AGGCAAAACTGGGCCCCATCGCGGGGACGTGGAAGGCCACTTGAGCTTCTCTGGAGAAGGACCTGA GGGACAAAGTCAACTCCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGCAGGAGCAGCAGGAGGATGCTGCTGCTGCTG CCTTGGAGAGCTGAGCTGCCCTGGTGG

EST11458 6	--	--	--	---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCAATTTCCACAGTGGT CCCATTAAACATTTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGCTTCCTTCCAGGTATTGTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATTTGCCGGCCCTCTCTGGGGCCCGTGG TCTCTCTGGTGTGGGTAGTCTCTGGAGTCAACGGTCTCTAGTGAAGCTGGTCTGTGATGGCAACC CTGGGAACGATGGTCCCCCAGGTGCGGATGGTCAACCCGGACACAAGGAGAGCGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAACCTGAAAAAGG CTGTCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTCTTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTCTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGACATGAAGGACCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGCGAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACCTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGGTTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGGAGAGAATATGGTCTCTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAAGTACTTGAAGTAAAGGAACTTGAATGTTATTCAACTGG ATTTCCAGTAGTTTCAGTTACTTATGAAATATTATGATACCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCCTAATTTGAATGATATTGCTGTGGGACCTGAGCACTTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGTTATTTGGGTTAGCGTGTGCTGATGTTGCTACTA TAGTCCAAGTGAA

EST10398 2	---	---	---	---	---	TGCTGGGGTGGCAAGGCTGCAAAAGAGGAGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTTACCAATTTGGGGCTTGACTTTCCACACGGAGAAAG CATTTGTTTCTTGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCAITTTG
EST36751 7	---	---	---	---	---	CCAAAGTCGTTCAATTTTAGCTTTGCAGGTTTAACTCGATTACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	---	---	---	---	---	CACGTGGAAGAGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGCCCCAAACTTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACCTGGATGCTTTAATAACAAATATTTTACCTTTTGAAAAAATAATG AAGGATTTGACCTGCTTGGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCTA
EST18288 3	---	---	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCAGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	---	---	---	---	---	TTCCCGCCAGCCCCCATCTTGGCACCTGGTCCCTCAGGGGCCACCCCGGCACTCACCGCTCT CGCTCTCGTTAACATCGGGCGGGCGCTCTTGAACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCGGGCTTGGCAGGGGCCAGCCCTGCAGAGAGGGGTCCTGCTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTTG
EST58707 7	---	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCCTAGAAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACTTCAACGATACCTGCTCTGTTAGGCCAGGTTTATAGCA CACTTGTCACTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6	---	---	---	---	---	AGACCATGAAGAGTTGAAGGCTACAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGAGCTGCAGGGCGGCGAGCCCGGCTGGGGCGGACATGGAGGA CGTGGCGGCGGCTGTGTCAGTACCGGGGGAGGTGCAGGCCATGCTGGCCAGAGCACCGGAGGAGC TGCGGGTGGGCTCGCTCCCACTGGCAAGCTGGTAAGCGGCTCCTC
EST43211 8	---	---	---	---	---	CGCCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAAAGCGOC TGGCAGTGTACAGGCGGGCGCGAGGGCGCGAGCGGCGCTCAGCGCCATCCGGAGAGGCGCTG GGGCCCCGTGGTGAACAGGGCGCGCTGGCGGCGCGCACTGTGGGCTC
EST36770 4	---	---	---	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCCCTCCGATAGGGCTGGGCTGACCAAAATATACTGGTTTCTGTTTCTCTTCTGATCAT TCTTACAAAGTTATCTCTTATTGGAAGGCCCTAAAGAGGCTTATG

EST26021 1	..	--	--	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTAGGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTTGTAAAGAGGAGCAAGAGAACATTCCTCTGCAGCACCTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCAATTATGTGACTGAACCGACCTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGCACAAGACAAAGCAAGGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAAATAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCCCAATTCACCTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTTCGGAATCCTCCTCTGAAAGTGCCCGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTGGGTGCATCCTAAGCTCT GAGAGCAACCTTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTCACACATTCAGAAAGAGGGGTGGTCAAGTGGGTGGTAGGTCCAGTAATCCA AGGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCCTATGGGATTGACITTTATTTCTCCATTGTCTTACCTTTACAGGTGTTAATATAGTGAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACAGAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACTTGGTGTACCTTTAATTACAAACCTAG CAGACGGAACCTGAACCTCAGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGG ATCCCAAGGCCAACTCCCGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGG CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAGCAAGAGAAAGAGGCCCCAGAAAT CACAGGTGGGCACGTCCGTCTACCGCCATCTCCCTTCTACGGGAATTTTCAGGGTAACT
EST74082 0	--	--	--	---	---	TCCAGGTGGCTGGACCCAGGCCCCAGCTCTGACAGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGCAGGCCACCTGGCTTACGCTGCTCAGCCCTGCTGCTGTCAC CCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAAGTGAACATGACATTCCTTTAGT GGATAGATGCACAAACACACAAGCCATTATGGGAAGGATCCAGGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCATTTAAACAGCCCTTATCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTGAAT

EST65258 8	--	--	---	---	TGCCCATCACCGCGGCGAGACATGGCTTGCACAGCTTTGAGGATGTACCAATTAAACCAGAAAT CCAGTTATTTCCACCCTCAAATGACAGCCATGGCGCGGGTGTCTCTGGGGCTCTCGGGGGG ACAGCTCCACTCTGACTGGCAGATCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	--	--	---	---	ATGCAGGATGAAGGTGGACAGGGGAGAGGGCCAACTGTATCCAGGGCTGCAGATGTCGCTG GACTATGGGTTTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 2	--	--	---	---	ATACTAGTACAAGTGGTAATTTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTTCTCGAAGTGCAGTATCCAGAGTTTGGTTTTTGAAC TAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGCTTGGGTTTTTGGTGCATGCA
EST35879 9	--	--	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTTGAAGACAGCAGCGGGATGGGGCAGGAGAAGCTGCTGGATGAA
EST68308 5	--	--	---	---	GGAAGAGATTTAAGAAGCTTGATTTGGACAAATCTGCTTCTTGTAGTGTGAAGAGTTTCACTCTCT GCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAACTAGACTTTAAAGGTAAAGATAGTATTTTTT
EST54045 6	--	--	---	---	GGAATATTAATAATTTTAAATACCTCCATTTGCTTATCCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGAAATCT GTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0	--	--	---	---	ATCACAGGTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGTGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST19590 2	--	--	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTGCGGCTCAGGAT GCCGGAATGAC
EST76136 2	--	--	---	---	TGAAGCTTCTGCCAGCTTGCAATTTCTTAGGAGAACCCGGCTCATACCTTTATCTATAGCCTTCCCC TAGGCTT
EST58607 0	--	--	---	---	CTCTGGATGGTTTCAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTTGGCTCC CAAGTTGCTCTCCTCACTGAGACAAGGACAGCCACATGGCGGGATGGCGGGGAGTCTGCTG TGCGCCACGGCTGTGGCTGTTGTGAACGGTAGCCCTTGGGTTGCGATGCCTAAACCTTTGTTCT TGGCCAAAGGAGGGCGGGTGGCCATGCCTGAGATGTAGATGGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.